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OM protein - protein search, using sw model

Run on: April 4, 2006, 14:26:09 ; Search time 165 Seconds
(without alignments)
625.478 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap.*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap.*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap.*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1268	100.0	247	3	US-09-840-989A-2
2	1268	100.0	247	3	US-09-361-736-10
3	1268	100.0	247	4	US-10-116-051-2
4	1268	100.0	247	4	US-10-177-293-441
5	1268	100.0	247	4	US-10-418-226-10
6	1268	100.0	247	4	US-10-465-572-18
7	1268	100.0	247	4	US-10-372-683-41
8	1268	100.0	247	4	US-10-614-990-2
9	1268	100.0	247	5	US-10-723-860-4202
10	1268	100.0	247	5	US-10-824-075-2
11	1268	100.0	247	6	US-11-068-678-3
12	1268	100.0	247	6	US-11-076-158-2
13	1268	100.0	247	6	US-11-125-206-10
14	937	73.9	276	3	US-09-925-300-1426
15	662.5	52.2	256	3	US-09-840-989A-3
16	662.5	52.2	256	4	US-10-614-990-3
17	660.5	52.1	204	4	US-10-116-051-10
18	660.5	52.1	204	6	US-11-076-158-10
19	628	49.5	170	3	US-09-361-736-9
20	628	49.5	170	4	US-10-418-226-9
21	628	49.5	170	6	US-11-125-206-9
22	358	28.2	70	3	US-09-864-761-37770
23	354	27.9	293	5	US-10-900-423-13
24	354	27.9	302	3	US-09-193-881-23
25	354	27.9	302	4	US-10-177-293-443
26	354	27.9	302	4	US-10-338-395-23
27	354	27.9	302	4	US-10-418-226-12

ALIGNMENTS

RESULT 1

US-09-840-989A-2
; Sequence 2, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Ti
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 3; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.6e-121; Indels 0; Gaps 0;
Matches 247; Conservative 0; Mismatches 0;

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Db	1	MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGAFACL	60
QY	61	ENSTCDTDMYDICKSFLYSAAKFDQGAFFVKESLKCIANGVTSKVFIAIRCSTFORM	120
Db	61	ENSTCDTDMYDICKSFLYSAAKFDQGAFFVKESLKCIANGVTSKVFIAIRCSTFORM	120
QY	121	IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSILLECDEDTVSTIRD	180
Db	121	IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSILLECDEDTVSTIRD	180
QY	181	SLMEKIGPNWASLFHILQTDHCAQTHPRADFNRRRTNEPQKLVLLNLRAGEEDSPSHIK	240
Db	181	SLMEKIGPNWASLFHILQTDHCAQTHPRADFNRRRTNEPQKLVLLNLRAGEEDSPSHIK	240
QY	241	RTSHESA 247	
Db	241	RTSHESA 247	

RESULT 2

US-09-361-736-10
; Sequence 10, Application US/09361736

Patent No. US20020102634A1
; GENERAL INFORMATION: US/10116051
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stannocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-10

Query Match 100.0%; Score 1368; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKCIIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKCIIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 3
US-10-116-051-2
; Sequence 2, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN

FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-051-2
Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKCIIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKCIIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 4
US-10-177-293-441
; Sequence 441, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavaru, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Aysegul
; APPLICANT: Sahin, Funda
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572

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; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 441
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-441
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Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTOGKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFDTOGKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120

QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDEDTVTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDEDTVTIRD 180

QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 5
US-10-418-226-10
; Sequence 10, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PFI43P102
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-10-418-226-10
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Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
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QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTOGKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFDTOGKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120

QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDEDTVTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDEDTVTIRD 180

QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 6
US-10-465-572-18
; Sequence 18, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-572-18
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Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTOGKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFDTOGKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120

QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDEDTVTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFNSRYNRLVRSLLCEDEDTVTIRD 180

QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 7
US-10-372-683-41
; Sequence 41, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
```

; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 41
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 8
US-10-614-990-2
; Sequence 2, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 9
US-10-723-860-4202
; Sequence 4202, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4202
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4202

Query Match 100.0%; Score 1268; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 10
US-10-824-075-2
; Sequence 2, Application US/10824075
; Publication No. US2005002629A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.,
; APPLICANT: HONGO, JO-ANNE S.
; APPLICANT: ZLOT, CONSTANCE H.

; APPLICANT: et al.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143PID3
; CURRENT APPLICATION NUMBER: US/11/125,206
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 10/418,226
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-11-125-206-10

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.6e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKESLKCIANGVTSKVFLAIRRCSTFORM 120

QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180

QY 181 SLMEKIGPNMASLFHIQTDHCAQTHPRADFNRRRTNBPQKVLNRLNRGDEDSFSHIK 240
DB 181 SLMEKIGPNMASLFHIQTDHCAQTHPRADFNRRRTNBPQKVLNRLNRGDEDSFSHIK 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 14
US-09-925-300-1426
; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (273)

W6 00 55174

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (275)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 3; Length 276;
Best Local Similarity 99.5%; Pred. No. 6.8e-87;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 89 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 148

QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 149 ENSTCDTGMVDICKSFLYSAAKFTQGFVKESLKCIANGVTSKVFLAIRRCSTFORM 208

QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
DB 209 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 268

QY 181 SLMEKI 186
DB 269 SLMEKI 274

RESULT 15
US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncozyrhynchus kisutch
US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 3; Length 256;
Best Local Similarity 53.4%; Pred. No. 6.4e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

QY 11 LVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTGM 70
DB 12 LVIGTAATFTDPEA-SPRRARFSSNSPSDVARCLNGALA VCGTGFACLENSTCDTGM 70

QY 71 YDICKSFLYSAAKFTQGFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQECYS 130
DB 71 HDICQLFHTAATNTQGTFFVKESLRCIANGVTSKVFTIRRCGVFORMIEVQECYS 130

QY 131 KLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRDSLMEKIGPNM 190
DB 131 RLIDICGVARSNPEAIGEVVQVPAHPNRYISTLLQSLACDEETVAVVRAGLVARLGPDM 190

QY 191 ASLPHILOTDHCAQTHPRADFN-----RRRTNEPQKLVLLNLRGDEDSPSHI 239
DB 191 ETLFOLLQNKHCPCQSNQGPSAPAGWPMGSPSPFKI-QPSMRGRD--PTH 241

Search completed: April 4, 2006, 14:29:48
Job time : 167 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 14:27:09 ; Search time 25 Seconds
(without alignments)
300.766 Million cell updates/sec

Title: US-09-703-350B-76

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /SIDSS/ptodata/2/pubppa/US06_NEW_PUB.pdb:*
- 2: /SIDSS/ptodata/2/pubppa/US06_NEW_PUB.pdb:*
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- 5: /SIDSS/ptodata/2/pubppa/US09_NEW_PUB.pdb:*
- 6: /SIDSS/ptodata/2/pubppa/US10_NEW_PUB.pdb:*
- 7: /SIDSS/ptodata/2/pubppa/US11_NEW_PUB.pdb:*
- 8: /SIDSS/ptodata/2/pubppa/US60_NEW_PUB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354	27.9	302	7	US-11-051-720-1458
2	308	24.3	187	7	US-11-051-720-1402
3	93.5	7.4	350	6	US-10-533-811-31
4	85.5	6.7	311	6	US-10-793-626-2460
5	83	6.5	319	6	US-10-793-626-792
6	83	6.5	319	6	US-10-793-626-2008
7	83	6.5	344	7	US-11-096-568A-27671
8	83	6.5	365	7	US-11-096-568A-27670
9	83	6.5	398	6	US-10-793-626-44
10	83	6.5	398	6	US-10-793-626-1498
11	82.5	6.5	1724	7	US-11-096-568A-32051
12	82.5	6.5	1730	7	US-11-096-568A-32050
13	82.5	6.5	1737	7	US-11-096-568A-32049
14	82.5	6.5	2535	7	US-11-096-568A-27511
15	81.5	6.4	2518	6	US-11-096-568A-27512
16	81	6.4	4384	6	US-10-821-234-1120
17	78.5	6.2	2376	7	US-11-096-568A-27513
18	77.5	6.1	762	6	US-10-204-639-21
19	76.5	6.0	1087	7	US-11-096-568A-27941
20	75.5	6.0	364	7	US-11-072-512-2127
21	75	5.9	357	7	US-11-072-512-2525
22	75	5.9	750	7	US-11-072-512-2432
23	75	5.9	1333	7	US-11-096-568A-27668
24	75	5.9	1351	7	US-11-096-568A-27667
25	75	5.9	1528	7	US-11-096-568A-27666

26	74.5	5.9	292	7	US-11-096-568A-10393
27	74.5	5.9	401	7	US-11-096-568A-10392
28	74.5	5.9	406	6	US-10-821-234-1113
29	74.5	5.9	698	7	US-11-038-901-2
30	74	5.8	625	7	US-11-072-512-2061
31	74	5.8	857	7	US-11-096-568A-24558
32	74	5.8	867	7	US-11-096-568A-24557
33	74	5.8	903	7	US-11-096-568A-24556
34	74	5.8	1149	7	US-11-110-082-30
35	73	5.8	1148	7	US-11-110-082-29
36	73	5.8	1373	7	US-11-096-568A-29856
37	73	5.8	1391	7	US-11-096-568A-29855
38	73	5.8	1568	7	US-11-096-568A-29854
39	72.5	5.7	224	7	US-11-096-568A-10357
40	72.5	5.7	278	7	US-11-096-568A-10356
41	72.5	5.7	292	7	US-11-096-568A-29657
42	72.5	5.7	292	7	US-11-096-568A-33082
43	72.5	5.7	402	7	US-11-096-568A-29656
44	72.5	5.7	402	7	US-11-096-568A-33081
45	72.5	5.7	414	7	US-11-096-568A-16419

ALIGNMENTS

RESULT 1

US-11-051-720-1458

; Sequence 1458, Application US/11051720

; Publication No. US20060046257A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHOD

; FILE REFERENCE: 1847.1002

; CURRENT APPLICATION NUMBER: US/11/051,720

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1780

; SEQ ID NO 1458

; LENGTH: 302

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-051-720-1458

Query Match 27.9%; Score 354; DB 7; Length 302;

Best Local Similarity 32.4%; Pred. No. 2.9e-27;

Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY	9	LVLVIS-----ASATHEAE-QNDSVSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB	12	LALVLATFDPARGTDATNPPEGQDRSSQKGRLSLQNTAEIQHCLVNLNAGDVGCVFECF 71
QY	61	ENSTCDTDCMYDICKSFLYSAKFDQGAFFVKESLKIANGVTYSKVFLLAIRRCSTFORM 120
DB	72	ENNSCEIRGLHGICMTFLHNAGKFDQGSFKDKALKCKAHLRHFGCISRKCPAREM 131
QY	121	IAEVQSECTSKLNVCSIAKRNPEAITVEVQLPNHFNRYNRLVRSLLCEDEPTVSTIRD 180
DB	132	VSQLQRECYLKHDLCAAQENTVIVEMIFKDLLLHEPVVDLVNLLTTCGEVKEAITH 191
QY	181	SLMEKIGPNNASLFIHLQ-TDHCQAQTHPRADFNRRRTNEPQKL----- 222
DB	192	SVQVQCEQNWGSLCSILSFACTSAIQKPPTAPPERPQVDRTKLSRAHHGAGHHLPEPSS 251
QY	223	KVLLRLNLRGEEDSPSH 238
DB	252	RETGRGAKGERGSKSH 267

RESULT 2

US-11-051-720-1402

; Sequence 1402, Application US/11051720

; Publication No. US20060046257A1

; GENERAL INFORMATION:

```
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1402
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1402

Query Match      24.3%; Score 308; DB 7; Length 187;
Best Local Similarity 37.6%; Pred. No. 5.3e-23;
Matches 59; Conservative 37; Mismatches 49; Indels 12; Gaps 3;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60
Db LALVLATFPDARGTDATNPPEGPQDRSSQKGRLSLQNTAEIQHCLVNAQDVGCGVFECF 71

QY 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
Db ENNSCEIRGLHGICWTFLEHAGKFDQAQGSFIKDKALKCAHALRHRFGCISRKCPAIREM 131

QY 121 IAEVQEECYKLVNCSIAKRNPEATEVTVQLPNHFNSN 157
Db VSQLORECYLKHDLCAAAQENTRVIVEMI-----HFMD 164

RESULT 3
US-10-533-811-31
; Sequence 31, Application US/10533811
; Publication No. US20060051364A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; HUMAN SERVICES
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Barral, Aldina
; APPLICANT: Netto, Mancel
; APPLICANT: Brodskyt, Claudia
; APPLICANT: Gomes, Regis
; TITLE OF INVENTION: LU. LONGIPALPIS POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 4239-67028-08
; CURRENT APPLICATION NUMBER: US/10/533,811
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/422,303
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/US2003/034453
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Lutomyia longipalpis
US-10-533-811-31

Query Match      7.4%; Score 93.5; DB 6; Length 350;
Best Local Similarity 21.4%; Pred. No. 0.16;
Matches 41; Conservative 39; Mismatches 73; Indels 39; Gaps 8;

QY 4 NSAVLLVLVISATHEAEQNDSVSPKSRVAQNSAEVVRCLNSALQVCGGAFACLENS 63
Db SSQSSSPVMTNKTKEFIRNEIQKVRKRVNFQETLQKIRDISAIAKKVSSSECLSNL 239

QY 64 T-----CUTDMYDICKSFLYSAAKFTDQKAFVKESLKCIANG--VTSKVFLAIRRCSTF 117
Db TDKGLVSDGINCLKEKF-----NDGRIILQYNNLLKGLKIPNDLWELKKCDTN 291

QY 118 Q-----RMAIEVQEECYKLVNCSIAKRNPEATEVTVQLPNHFNSR-----YYNRLVRS 166
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Db 292 QNNTLGRIL-----CYF-LTPLOLEK-----EQILLPVEFIKRILELTHYFSTMKED 337
QY 167 LLECEDETVSTI 178
Db 338 LINCGITTIASI 349

RESULT 4
US-10-793-626-2460
; Sequence 2460, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2460
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2460
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Query Match      6.7%; Score 85.5; DB 6; Length 311;
Best Local Similarity 25.6%; Pred. No. 0.83;
Matches 42; Conservative 21; Mismatches 21; Indels 31; Gaps 6;

QY 35 AAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDMY-----DICK 75
Db 15 SAEKLAETIINLESILELPKGT---EHFVSDLHGEYESFQHLRNGSGNVRRAKINDIFK 70

QY 76 SFLYSAAKFTDQKAFV-KESLKCIANGVTSKVFLAIRRCSTFORMIAIEVQEECYSKLVN 134
Db 71 DKLSQOEINDLAALVYYPEEKLKLVKNFDSIGTLNIWYITTIQRLI-DLITYCSSKYTR 129

QY 135 CSAIKRNPE---ALTEVVQLPNHFNSR--YYNRLVRSILLEDE 172
Db 130 SKLRALPEQYVYIIIEELLYKSNFHNKPKYPYETLVNQIIIELEQ 173
```

```
RESULT 5
US-10-793-626-792
; Sequence 792, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 792
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-792

Query Match      6.5%; Score 83; DB 6; Length 319;
Best Local Similarity 19.5%; Pred. No. 1.5;
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Db 141 CLHRSFAQSSVSDVSDSNCSTGSDCANRT-----CIAH-----SLFG 180
Qy 119 RMIAEVOECYKLNVCSTAKRNPETVQLPNHFSNRYNRLVRSLLCEDETVSTI 178
Db 181 MDIFE-QLNCYS-----CGLESRH-----LKYTSFFHINASALRTWKVTCARNSF--- 225
Qy 179 RDLMEKIGPNNASLFIHLQTD 200
Db 226 -DELL-----NLVEMNHQLACD 241

RESULT 9
US-10-793-626-44
; Sequence 44, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-44

Query Match 6.5%; Score 83; DB 6; Length 398;
Best Local Similarity 22.6%; Pred. No. 2;
Matches 44; Conservative 32; Mismatches 57; Indels 62; Gaps 11;
Qy 57 FACLENSTCDTD-----GMVDICKSFLYSAAKFDTOGKAFVKESLKIANGVTSKVFLAI 111
Db 247 FIKFEATIEDTHTSKQGLYDVIOFSF---KDKVTEGKSFYRLNVR-----INSEDIAP 298
Qy 112 RRCSTFORMIAEVOECYKLNVCSTAKRNPETVQLPNHFSNRYNRLVRSLLCED 171
Db 299 QDLIQLKEMITEFEEN-----ENQFV--FIEDLNLQYVQND 332
Qy 172 EDTVSTIRDSLMKIGPNM---ASLPHILOTDHCAQTHPRA-----DFNR-----RRTNEP 219
Db 333 EMPI-----VKFSPPELLDDASLFDSAMTD--LYLNPRASKFLDDYNEFDKVELVNHA 383
Qy 220 QKLKVLRLNRGEED 234
Db 384 ERL--LKDEMGRGEQN 396

RESULT 10
US-10-793-626-1498
; Sequence 1498, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1498
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1498

Query Match 6.5%; Score 83; DB 6; Length 398;
Best Local Similarity 22.6%; Pred. No. 2;
Matches 44; Conservative 32; Mismatches 57; Indels 62; Gaps 11;
Qy 57 FACLENSTCDTD-----GMVDICKSFLYSAAKFDTOGKAFVKESLKIANGVTSKVFLAI 111
Db 247 FIKFEATIEDTHTSKQGLYDVIOFSF---KDKVTEGKSFYRLNVR-----INSEDIAP 298
Qy 112 RRCSTFORMIAEVOECYKLNVCSTAKRNPETVQLPNHFSNRYNRLVRSLLCED 171
Db 299 QDLIQLKEMITEFEEN-----ENQFV--FIEDLNLQYVQND 332
Qy 172 EDTVSTIRDSLMKIGPNM---ASLPHILOTDHCAQTHPRA-----DFNR-----RRTNEP 219
Db 333 EMPI-----VKFSPPELLDDASLFDSAMTD--LYLNPRASKFLDDYNEFDKVELVNHA 383
Qy 220 QKLKVLRLNRGEED 234
Db 384 ERL--LKDEMGRGEQN 396

RESULT 11
US-11-096-568A-32051
; Sequence 32051, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32051
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1724)
; OTHER INFORMATION: Ceres Seq. ID no. 13592046
US-11-096-568A-32051

Query Match 6.5%; Score 82.5; DB 7; Length 1724;
Best Local Similarity 24.4%; Pred. No. 16;
Matches 49; Conservative 24; Mismatches 55; Indels 73; Gaps 11;
Qy 66 DTDGMVDICKSFLYSAA---KFDTOGK-----AFVKESLKCI-----ANGVTSK 106
Db 360 DEEGWLDITTSLSWEAATLLKPDTSKSGMDPGGYVK--VKCIPGRRSESMVVGKGVCK 417
Qy 107 VFLAIRRCSST-----FORMIAEV-----OBECYKLNVCSTAKRNP 143
Db 418 KNVAHRMTSKIEKPRLLILGALLSYQRISNQLSSFDTLQDEMHLKXAVAKIDSHNPD 477
Qy 144 ATTEVVQLPNHFSNRYNRLVRSLLCEDEDTVTSTIRDSLMKEI-----G 187
Db 478 -ILLVEKSVSRFAQEV-----LLAKDISLVNLIKRSLLERISRCTGAQIVPSIDLTS 529
Qy 188 PNM--ASLPHILOTDHCAQTH 206
Db 530 PKLGYCDLPHV---EKFVETH 547

RESULT 12
US-11-096-568A-32050
; Sequence 32050, Application US/11096568A
; Publication No. US20060048240A1
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1498

Query Match 6.5%; Score 83; DB 6; Length 398;
Best Local Similarity 22.6%; Pred. No. 2;
Matches 44; Conservative 32; Mismatches 57; Indels 62; Gaps 11;
Qy 57 FACLENSTCDTD-----GMVDICKSFLYSAAKFDTOGKAFVKESLKIANGVTSKVFLAI 111
Db 247 FIKFEATIEDTHTSKQGLYDVIOFSF---KDKVTEGKSFYRLNVR-----INSEDIAP 298
Qy 112 RRCSTFORMIAEVOECYKLNVCSTAKRNPETVQLPNHFSNRYNRLVRSLLCED 171
Db 299 QDLIQLKEMITEFEEN-----ENQFV--FIEDLNLQYVQND 332
Qy 172 EDTVSTIRDSLMKIGPNM---ASLPHILOTDHCAQTHPRA-----DFNR-----RRTNEP 219
Db 333 EMPI-----VKFSPPELLDDASLFDSAMTD--LYLNPRASKFLDDYNEFDKVELVNHA 383
Qy 220 QKLKVLRLNRGEED 234
Db 384 ERL--LKDEMGRGEQN 396

RESULT 11
US-11-096-568A-32051
; Sequence 32051, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32051
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1724)
; OTHER INFORMATION: Ceres Seq. ID no. 13592046
US-11-096-568A-32051

Query Match 6.5%; Score 82.5; DB 7; Length 1724;
Best Local Similarity 24.4%; Pred. No. 16;
Matches 49; Conservative 24; Mismatches 55; Indels 73; Gaps 11;
Qy 66 DTDGMVDICKSFLYSAA---KFDTOGK-----AFVKESLKCI-----ANGVTSK 106
Db 360 DEEGWLDITTSLSWEAATLLKPDTSKSGMDPGGYVK--VKCIPGRRSESMVVGKGVCK 417
Qy 107 VFLAIRRCSST-----FORMIAEV-----OBECYKLNVCSTAKRNP 143
Db 418 KNVAHRMTSKIEKPRLLILGALLSYQRISNQLSSFDTLQDEMHLKXAVAKIDSHNPD 477
Qy 144 ATTEVVQLPNHFSNRYNRLVRSLLCEDEDTVTSTIRDSLMKEI-----G 187
Db 478 -ILLVEKSVSRFAQEV-----LLAKDISLVNLIKRSLLERISRCTGAQIVPSIDLTS 529
Qy 188 PNM--ASLPHILOTDHCAQTH 206
Db 530 PKLGYCDLPHV---EKFVETH 547

RESULT 12
US-11-096-568A-32050
; Sequence 32050, Application US/11096568A
; Publication No. US20060048240A1
```

GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32050
; LENGTH: 1730
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1730)
; OTHER INFORMATION: Ceres Seq. ID no. 13592045
US-11-096-568A-32050

Query Match 6.5%; Score 82.5; DB 7; Length 1730;
Best Local Similarity 24.4%; Pred. No. 16;
Matches 49; Conservative 24; Mismatches 55; Indels 73; Gaps 11;

QY 66 DTGMYDICKSFYLSAA---KFTQCK-----AFVKESLKC-----ANGVTSK 106
DB 366 DEEGWLDIITSLSWEAATLLKPDTSKGGMDPGGYK--VKCIPCGRRSESVMVKGVCK 423
QY 107 VFIAIRRCST-----FORMIAEV-----QBECKSLNVCIAKNPE 143
DB 424 KNVAHRMTSKIEKPRLLILGGALEYQRIQNQLSSFDTLQEQMDHLKMAVAKIDSHNPD 483
QY 144 AITEVVQLPNHFSNRYNRLVRSLLCEDETVSTIRDSLMKEI-----G 187
DB 484 -ILLVKSVSRAQY-----LLAKDISLVNKRSLRISRCTGAQIVPSIDQLTS 535

QY 188 PNM--ASLPHILOTDHCAQTH 206
DB 536 PKLGYCDLFHV---EKFVEITH 553

RESULT 13
US-11-096-568A-32049
; Sequence 32049, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32049
; LENGTH: 1757
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1757)
; OTHER INFORMATION: Ceres Seq. ID no. 13592044
US-11-096-568A-32049

Query Match 6.5%; Score 82.5; DB 7; Length 1757;
Best Local Similarity 24.4%; Pred. No. 16;
Matches 49; Conservative 24; Mismatches 55; Indels 73; Gaps 11;

QY 66 DTGMYDICKSFYLSAA---KFTQCK-----AFVKESLKC-----ANGVTSK 106
DB 393 DEEGWLDIITSLSWEAATLLKPDTSKGGMDPGGYK--VKCIPCGRRSESVMVKGVCK 450
QY 107 VFIAIRRCST-----FORMIAEV-----QBECKSLNVCIAKNPE 143
DB 451 KNVAHRMTSKIEKPRLLILGGALEYQRIQNQLSSFDTLQEQMDHLKMAVAKIDSHNPD 510

QY 144 AITEVVQLPNHFSNRYNRLVRSLLCEDETVSTIRDSLMKEI-----G 187
DB 511 -ILLVKSVSRAQY-----LLAKDISLVNKRSLRISRCTGAQIVPSIDQLTS 562

QY 188 PNM--ASLPHILOTDHCAQTH 206
DB 563 PKLGYCDLFHV---EKFVEITH 580

RESULT 14
US-11-096-568A-27511
; Sequence 27511, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27511
; LENGTH: 2535
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2535)
; OTHER INFORMATION: Ceres Seq. ID no. 1819121
US-11-096-568A-27511

Query Match 6.5%; Score 82.5; DB 7; Length 2535;
Best Local Similarity 15.9%; Pred. No. 27;
Matches 53; Conservative 58; Mismatches 91; Indels 131; Gaps 13;

QY 12 VISASATHEAEOND---SVSPKRSVAAQNSAEVVRCLNSALQVGGCAACLENSTCDTD 68
DB 17 VMAFRPSHEAKLRELLHNICLHEIKLCSDAAKEFVKLLKG-----ETG 59

QY 69 GMVDICKSFLYSAAKF-----DTQKAFVKESLKCIA-----GVTSKVFLAIRRC 114
DB 60 G--DLLRYFQSPNPAEELLEAWKLHEKQGLSYFSLIQTILSHPEGKDRSTDIG-RAI 116

QY 115 STFORMIAEVQ--EECYSKLN-----VCSIAKNPEAITEVV-----149
DB 117 DQFGLLVEEKLDIIYKELNSKEGKQSAALSILASIVRRGPGMASEIAKKDFKGFAXL 176

QY 150 -----OLPNHFSNR-----YNNRLVRSLLCEDEDT 174
DB 177 AEYNTQGTETKVKKHSTRKAFVGFSAISFLEVBKPGLLSSVLNKKEMYSKVLPGLGKDDDDT 236

QY 175 VSTIRDSLMKE-----IGPNMAS-LPHILOTDHCAQTHPR-----208
DB 237 VASVLSTLKDKILVEESLISPGLSRVLFGLVTILKHLASISAREDAIVNELAHDVLVKVC 296

QY 209 -----ADFNRRRTNEPQKLKVLRLNLRGEE 233
DB 297 TDPNSGLMPDAKKLKGNSDRLLMLMKGLRAAE 329

RESULT 15
US-11-096-568A-27512
; Sequence 27512, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27512

```
; LENGTH: 2518
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2518)
; OTHER INFORMATION: Ceres Seq. ID no. 1819122
US-11-096-568A-27512

Query Match      6.4%; Score 81.5; DB 7; Length 2518;
Best Local Similarity 19.4%; Pred. No. 33;
Matches 49; Conservative 38; Mismatches 80; Indels 85; Gaps 10;

QY 20 EAEQNDVSPRKSRVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTGMVDICKSFLY 79
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 108 EKLDLDIYKELNSKEGKQOSA-ALSLLASIVRRGPGMAS-----EIAKKFDF 153
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 80 SA-----AKFTDQGAFFVESLKCICANGVTSKVFLAIRRCSTFQRMIAEVQEBCYCKLNVC 135
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 154 KGFAKLAERYNTQGTETKVKKH-----STRKAPVGF-----AISFL 187
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 136 SIAKRNPETATEVQVLPNHFNSRNYNRLVRSLLCEDTETVSTIRDSLMK-----IGP 188
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 188 EVCK--PGLSSVLN-----KKEMYSKVLPGLGKDDDDTVASVLTLDKILVEESLISP 240
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 NMAS-LFHILQTDHCAQTHPR-----ADFNRRRTNEPOK 221
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 GLRSVLFGIIVTLKHLASISAREDAIGIVNELAHDVLVKVCTDPFNGMLMPDAKRLRGNSDR 300
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 222 LKVLRLNLRGEE 233
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 LLMLMKGLRAAE 312
```

Search completed: April 4, 2006, 14:30:18
Job time : 26 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 14:07:08 ; Search time 189 Seconds
(without alignments)
574.215 Million cell updates/sec

Title: US-09-703-350b-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	AAR84522	Aar84522 Stannioa
2	1268	100.0	247	AAB23264	Aab23264 Human sta
3	1268	100.0	247	AAV55750	Aay55750 Human sta
4	1268	100.0	247	AAV57166	Aay57166 Human cor
5	1268	100.0	247	AAV92901	Aay92901 Human sta
6	1268	100.0	247	AAB62473	Aab62473 Human sta
7	1268	100.0	247	AAB62690	Aab62690 Lng108, a
8	1268	100.0	247	ABO84399	Abb6259 Human sta
9	1268	100.0	247	ABP97748	Abp97748 Amino aci
10	1268	100.0	247	ABR47600	Abp97748 Breast ca
11	1268	100.0	247	ABG72290	Abg72290 Human Cor
12	1268	100.0	247	ADDA48082	Add48082 Human Pro
13	1268	100.0	247	ADI30575	Adi30575 Human sta
14	1268	100.0	247	ABO84399	Abb6259 Human sta
15	1268	100.0	247	ADQ21382	Adq21382 Human sof
16	1268	100.0	247	ABR87637	Abp97748 Human sta
17	1268	100.0	247	ABO81112	Abp97748 Human sta
18	1268	100.0	255	ABE54713	Aeb54713 Human sta
19	1234	97.3	247	ABE08116	Aeb08116 Mouse sta
20	1231	97.1	247	ADD48080	Add48080 Rat Prote
21	937	73.9	276	3 AAB56848	Aab56848 Human pro
22	680.5	53.7	261	1 AAP82968	Aap82968 Corpuscle
23	662.5	52.2	256	4 AAB62474	Aab62474 Coho salm
24	628	49.5	170	3 AAY55749	Aay55749 A. austria

25	628	49.5	170	7	ADI30574	Adi30574 Australia
26	358	28.2	70	4	AAM18134	Aam18134 Peptide #
27	358	28.2	70	4	ABB37166	Abb37166 Peptide #
28	358	28.2	70	4	AAM30637	Aam30637 Peptide #
29	358	28.2	70	4	ABB31928	Abb31928 Peptide #
30	358	28.2	70	4	ABB22472	Abb22472 Protein #
31	358	28.2	70	4	AAM70300	Aam70300 Human bon
32	358	28.2	70	4	AAM57878	Aam57878 Human bra
33	358	28.2	70	4	ABG52000	Abg52000 Human liv
34	358	28.2	70	4	AAM05763	Aam05763 Peptide #
35	358	28.2	70	5	ABG39940	Abg39940 Human pep
36	354.5	28.0	296	3	AAV67926	Aay67926 Mouse sta
37	354.5	28.0	296	4	AAB61623	Aab61623 Murine st
38	354.5	28.0	296	9	ABE08118	Aeb08118 Mouse sta
39	354	27.9	293	2	AAV41255	Aay41255 Adipogene
40	354	27.9	293	3	AAB26872	Aab26872 Human adi
41	354	27.9	293	4	AAB93965	Aab93965 Human pro
42	354	27.9	302	3	AAV67925	Aay67925 Human sta
43	354	27.9	302	4	AAB98971	Aab98971 Human adi
44	354	27.9	302	4	AAB61621	Aab61621 Human sta
45	354	27.9	302	4	AAB31797	Aab31797 Amino aci

ALIGNMENTS

RESULT 1
AAR84522
ID AAR84522 standard; protein; 247 AA.
XX
AC AAR84522;
XX
DT 19-APR-1996 (first entry)
XX
DE Stannioalcin from Corpuscles of Stannius.
XX
KW stannioalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..33
FT Protein /label= prepro_region
FT /label= mature_stannioalcin
XX
PN WO9524411-A1.
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US005136.
XX
PR 08-MAR-1994; 94US-002080005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen H, Adams MD;
XX
DR WPI; 1995-328227/42.
XX
DR N-PSDB; AAT02438.
XX
PT Human corpuscles of Stannius polypeptide(s) - used to treat
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders.
XX
PS Claim 14; Fig 1; 4lpp; English.
XX
CC Stannioalcin, a Corpuscles of Stannius polypeptide is encoded by
CC AAT02438. Stannioalcin functions as a hypocalcaemic agent, and can be
CC used for the treatment of e.g. electrolyte disorders which lead to renal,
CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
CC to elevated bone resorption, e.g. osteoporosis and Paget's disease
XX

SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPPEATTEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPPEATTEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRTNEPQKLKVLRLNRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRTNEPQKLKVLRLNRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
RESULT 2
AAB23264
ID AAB23264 standard; protein; 247 AA.
XX AAB23264;
AC AAB23264;
XX 02-FEB-2001 (first entry)
DT 02-FEB-2001 (first entry)
DE Human stannioalcalcin.
XX Human; stannioalcalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy.
XX Homo sapiens.
OS JP2000229880-A.
PN 22-AUG-2000.
XX 10-FEB-1999; 99JP-00033262.
XX 10-FEB-1999; 99JP-00033262.
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX WPI; 2000-605236/58.
XX N-PSDB; AAB97594.
XX An osteogenesis promotor useful in the prevention and/or treatment of
PT bone diseases such as osteoporosis.
XX Example 1; Page 5-6; 6pp; Japanese.
XX The invention relates to a novel osteogenesis-promoting composition which
CC contains stannioalcalcin (STC) as the active component. Stannioalcalcin is a
CC possible regulator of mineral metabolism. The composition is useful as a
CC prophylactic and/or therapeutic agent for bone diseases such as
CC osteoporosis. The present sequence represents human stannioalcalcin which
CC was used in an exemplification of the invention
XX SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPPEATTEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPPEATTEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRTNEPQKLKVLRLNRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRTNEPQKLKVLRLNRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
RESULT 3
AAV55750
ID AAV55750 standard; protein; 247 AA.
XX AAV55750;
AC AAV55750;
XX 11-FEB-2000 (first entry)
DT 11-FEB-2000 (first entry)
DE Human stannioalcalcin polypeptide.
XX Stannioalcalcin-alpha polypeptide; teleocalcin; hypocalcin; hypocalcemic;
KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
KW electrolyte disorder; renal; heart disease; osteopetrosis; human;
KW Paget's disease; hypercalcemia.
XX Homo sapiens.
OS US5994103-A.
PN 30-NOV-1999.
XX 02-JUN-1995; 95US-00460529.
XX 10-NOV-1994; 94WO-US013206.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Fleischmann RD, Oleen HS;
XX WPI; 2000-038260/03.
XX Isolated nucleic acids encoding human stannioalcalcin-alpha useful for
PT treating electrolyte disorders which lead to renal, bone and heart
PT diseases, osteoporosis and Paget's disease.
XX Disclosure; Fig 3; 21pp; English.
XX The invention provides a human stannioalcalcin-alpha polypeptide (also
CC called teleocalcin and hypocalcin). Stannioalcalcin-alpha is an anti-
CC hypercalcemic glycoprotein hormone produced by the corpuscles of
CC stannius. It has a similar reported biological activity to that of
CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
CC in mammals. They exert hypercalcemic activity due to stimulation of bone
CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
CC at low doses it increases bone formation and at high doses it increases
CC bone reabsorption. Accordingly, human stannioalcalcin-alpha and antagonists
CC of it (under different circumstances) may be used to treat osteoporosis.
CC The DNA may be used to produce human stannioalcalcin-alpha according to
CC standard recombinant DNA methodologies. The human stannioalcalcin-alpha may
CC be produced either in vitro in a fermentation culture or in vivo as part
CC of a gene therapy protocol, and may be used to treat electrolyte

disorders which lead to renal, bone and heart diseases. Due to the biphasic nature of stanniocalcin-alpha it may be used to treat osteoporosis, osteopetrosis and Paget's disease. Alternatively, the polypeptides may be used as antigens in the production of antibodies to stanniocalcin-alpha and to assay for agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of stanniocalcin-alpha and may be used to treat osteoporosis and hypercalcemia. The present sequence represents a human stanniocalcin

Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAKFTQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAKFTQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQVLPNHFNSNRYNRLVRSLLCEDTSTTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQVLPNHFNSNRYNRLVRSLLCEDTSTTIRD 180
QY 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 4
AAY57166
ID AAY57166 standard; protein; 247 AA.
XX AC
XX AAY57166;
DT 11-FEB-2000 (first entry)
XX Human corpuscles of stanius polypeptide.
XX Corpuscles of stanius polypeptide; calcium; inhibition; human; renal; therapeutic; bone; heart disease; hypocalcemia; osteoporosis.
XX Homo sapiens.
XX US5994301-A.
XX 30-NOV-1999.
XX 28-APR-1995; 95US-00431117.
XX 08-MAR-1994; 94US-00208005.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Adams MD, Olsen HS;
XX WPI; 2000-038269/03.
XX N-PSDB; AA239520.
XX Human corpuscles of stanius polypeptides used to inhibit calcium uptake.
XX Claim 4; Fig 1A-B; 23pp; English.
XX This represents a human corpuscles of stanius polypeptide, having a calcium uptake inhibitory activity. The cDNA is deposited under the accession number ATCC Deposit No. 75652. The polypeptide can be used in a

method for the treatment of a patient having need to inhibit uptake of calcium. The method is also used for the therapeutic treatment of renal, bone, and heart diseases, and the antagonist (may be an antibody) may be used for treating hypocalcemia, and osteoporosis

Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAKFTQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAKFTQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQVLPNHFNSNRYNRLVRSLLCEDTSTTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQVLPNHFNSNRYNRLVRSLLCEDTSTTIRD 180
QY 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 5
AAY92901
ID AAY92901 standard; protein; 247 AA.
XX AC
XX AAY92901;
DT 26-SEP-2000 (first entry)
XX Human stanniocalcin protein.
XX PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation; adipocyte; obesity; diabetes; hypertension; heart disease.
XX Homo sapiens.
XX WO200016795-A1.
XX 30-MAR-2000.
XX 17-SEP-1999; 99WO-JP005080.
XX 17-SEP-1998; 98JP-00263004.
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;
XX WPI; 2000-283445/24.
XX N-PSDB; AAA11145.
XX Treating or preventing obesity, which is a risk factor for diabetes, hypertension and heart disease, comprises administering an agent containing stanniocalcin.
XX Example 1; Page 16; 19pp; Japanese.
XX This sequence represents the human stanniocalcin protein. Stanniocalcin is an inhibitor of the differentiation and maturation of adipocytes. The protein is used for preventing and treating obesity which is a risk factor for diabetes, hypertension, and heart disease. The coding sequence was isolated from IMR-90 cells

```
XX SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAQAQNSAEVVRCLNSALQVCGCAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAQAQNSAEVVRCLNSALQVCGCAFACL 60

QY 61 ENSTCDTGMVDICKSFLYSAKFTQGAQFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAKFTQGAQFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120

QY 121 IAEVQECYKLVNCSIAKRNPETAITEVVLQNFHFSNRYNRLVRSLLCEDTSTVSTIRD 180
DB 121 IAEVQECYKLVNCSIAKRNPETAITEVVLQNFHFSNRYNRLVRSLLCEDTSTVSTIRD 180

QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 6
AAB62473
ID AAB62473 standard; protein; 247 AA.
XX AAB62473;
XX 09-JUL-2001 (first entry)
XX Human stanniocalcin (STC) protein.
DE Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
XX antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW antiaustatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW hemostatic; thrombolytic.
XX Homo sapiens.
XX WO200130969-A2.
XX 03-MAY-2001.
XX 20-OCT-2000; 2000WO-US029432.
XX 27-OCT-1999; 99US-0161740P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UYHE-) UNIV HELSINKI.
XX Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M;
PI Andersson LC;
XX WPI; 2001-308626/32.
DR N-PSDB; AAF83297.
XX Novel composition useful for treating or protecting neural cells, for
PT treating Addison's disease, organ rejection, hyperproliferative disorder,
PT cancer, AIDS, multiple sclerosis, comprises stanniocalcin polypeptide.
XX Claim 1; Fig 1A-C; 253pp; English.
PS The invention relates to a human stanniocalcin (STC) polypeptide. A
CC pharmaceutical composition comprising the STC is useful for treating a
CC patient in need of increased levels of STC activity. STC and its
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CC modulators are useful for treating disorders or abnormalities of nervous
CC system, cerebrovascular diseases, dementia, encephalitis, central nervous
CC system infections or neoplasms, demyelinating diseases,
CC encephalomyelitis, spinal cord diseases, neuromuscular diseases such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as psoriasis, Gaucher's disease, cardiovascular diseases such as
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangioma, peoriasis, angiofibroma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the human
CC STC polypeptide
XX SQ Sequence 247 AA;
```

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Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAQAQNSAEVVRCLNSALQVCGCAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAQAQNSAEVVRCLNSALQVCGCAFACL 60

QY 61 ENSTCDTGMVDICKSFLYSAKFTQGAQFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAKFTQGAQFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120

QY 121 IAEVQECYKLVNCSIAKRNPETAITEVVLQNFHFSNRYNRLVRSLLCEDTSTVSTIRD 180
DB 121 IAEVQECYKLVNCSIAKRNPETAITEVVLQNFHFSNRYNRLVRSLLCEDTSTVSTIRD 180

QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRTNEPQKLVLLNLRGEEDSPSHIK 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247
```

```
RESULT 7
AAB62690
ID AAB62690 standard; protein; 247 AA.
XX AAB62690;
XX 06-AUG-2001 (first entry)
XX Lng108, a diagnostic marker for cancer.
DE Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
XX Homo sapiens.
XX WO200132209-A1.
XX 10-MAY-2001.
XX 03-NOV-2000; 2000WO-US030482.
XX 04-NOV-1999; 99US-0163444P.
XX (DIAD-) DIADEXUS INC.
XX
```


PI Recipon H, Macina RA, Chen S, Sun Y;
XX WPI, 2001-316386/33.
DR N-P5DB; AAF83823.
XX
XX Novel assay for diagnosing and monitoring cancer, involves determining
PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT comparing with control.
XX
XX Disclosure; Page 33-34; 36pp; English.
PS
XX The invention relates to diagnosing the presence of cancer or diagnosing
CC metastases of cancer in a patient that involves determining levels of
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC comparing the determined levels with levels of Lng108 a normal human
CC control. The method is useful for diagnosing the presence of cancer, and
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC monitoring a change in stage of the cancer, in a patient. A therapeutic
CC agent which is an antibody labeled with paramagnetic ions or a
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC cancer in a patient. A molecule which downregulates the expression or
CC activity of Lng108, is useful for treating cancer in a patient. Lng108
CC protein is useful for inducing an immune response against a target cell
CC expressing Lng108. The present sequence represents the human Lng108
CC polypeptide
XX
XX Sequence 247 AA;
SQ

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAQKAFVKSCLKCIANGVTSKVFLAIRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAQKAFVKSCLKCIANGVTSKVFLAIRCSTFORM 120
QY 121 IAEVQECYKLVNVCISIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTIRD 180
DB 121 IAEVQECYKLVNVCISIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTIRD 180
QY 181 SLMEKIGPNWASLFILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGRGSDSPSHIK 240
DB 181 SLMEKIGPNWASLFILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGRGSDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 8
ABB06259
ID ABB06259 standard; protein; 247 AA.
XX
XX ABB06259;
XX
XX 23-MAY-2002 (first entry)
XX
XX Human staniocalcin 1 protein.
XX
XX Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans.
XX
XX Homo sapiens.
OS
XX WO200204013-A1.
PN
XX 17-JAN-2002.
PD

XX 10-JUL-2001; 2001WO-JP005962.
XX
XX 11-JUL-2000; 2000JP-00209926.
XX
XX (BMLB-) BML INC.
XX
XX Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;
PI
XX WPI, 2002-164600/21.
DR N-P5DB; ABL40225.
XX
XX Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing staniocalcin I.
XX
XX Claim 2; Fig 1; 24pp; Japanese.
XX
XX The present invention describes an agent containing staniocalcin 1,
CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence represents human staniocalcin 1
XX
XX Sequence 247 AA;
SQ

Query Match 100.0%; Score 1268; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAQKAFVKSCLKCIANGVTSKVFLAIRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAQKAFVKSCLKCIANGVTSKVFLAIRCSTFORM 120
QY 121 IAEVQECYKLVNVCISIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTIRD 180
DB 121 IAEVQECYKLVNVCISIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTIRD 180
QY 181 SLMEKIGPNWASLFILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGRGSDSPSHIK 240
DB 181 SLMEKIGPNWASLFILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGRGSDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 9
ABP97748
ID ABP97748 standard; protein; 247 AA.
XX
XX ABP97748;
XX
XX 28-MAY-2003 (first entry)
XX
XX Amino acid sequence of human STC1 polypeptide.
XX
XX Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
KW follicular development; CA9; HXB; IGFBP5; HFARP; STC1; mi9-6; SSR4;
KW cancer.
XX
XX Homo sapiens.
OS
XX WO2003010205-A1.
PN
XX

PD 06-FEB-2003.
XX
XX 26-JUL-2002; 2002WO-US023786.
XX
XX 26-JUL-2001; 2001US-0307600P.
XX 24-JUL-2002; 2002US-00201642.
XX
XX (UYDU-) UNIV DUKE MEDICAL CENT.
XX
XX Riggins GJ, Lal A;
XX
XX WPI; 2003-239423/23.
XX N-PSDB; AB277288.
XX
XX Inhibiting angiogenesis for treating wound healing, retinopathy,
XX ischemia, inflammation, microvasculopathy, bone healing, skin
XX inflammation or follicular development by providing to a subject an
XX antisense polynucleotide.
XX
XX Claim 4; Page 61; 66pp; English.
XX
XX The present sequence is a human STC1 polypeptide. It is used in the
XX method of the invention. The specification describes a method modulating
XX angiogenesis associated with wound healing, retinopathy, ischemia,
XX inflammation, microvasculopathy, bone healing, skin inflammation or
XX follicular development. The method comprises providing to a subject HOG3,
XX HOG8, HOG18, CA9, HXB, IGFBP5, HFRP, STC1, mig-6 or SSR4. The methods,
XX antisense polynucleotides, polypeptides and antibodies are useful for
XX treating wound healing, retinopathy, ischemia, inflammation,
XX microvasculopathy, bone healing, skin inflammation or follicular
XX development, or cancer such as breast, colon or lung cancer, or
XX glioblastoma
XX
XX Sequence 247 AA;
XX
Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123; Indels 0; Gaps 0;
Matches 247; Conservative 0; Mismatches 0;
QY 1 MLQNSAVLLVLVISATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFFVKESLKCANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFFVKESLKCANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAITEVQLPNHFNSRNYNRLVRSLLCEDETVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAITEVQLPNHFNSRNYNRLVRSLLCEDETVSTIRD 180
QY 181 SLMEKIGPNWASLFHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNWASLFHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
RESULT 10
ABR47600
ID ABR47600 standard; protein; 247 AA.
XX
XX ABR47600;
XX
XX 12-JUN-2003 (first entry)
XX
XX Breast cancer associated protein sequence SEQ ID NO:441.
XX
XX Human; breast cancer; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX

XX WO2003004989-A2.
XX
XX 16-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019669.
XX
XX 21-JUN-2001; 2001US-0299887P.
XX 27-JUN-2001; 2001US-0301572P.
XX 18-JUL-2001; 2001US-0306501P.
XX 25-SEP-2001; 2001US-0325002P.
XX 05-MAR-2002; 2002US-0362585P.
XX 14-MAY-2002; 2002US-0380391P.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
XX Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
XX Bast RC, Hortobagyi GN, Pusztai L, Metc F, Sahin A, Mills GB;
XX
XX WPI; 2003-210381/20.
XX N-PSDB; ACC50301.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
XX of a marker in a patient sample with that in the control non-breast
XX cancer sample.
XX
XX Claim 1; SEQ ID NO 441; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
XX is afflicted with breast cancer. The method comprises comparing the level
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
XX ABR47386 to ABR47632) in a patient sample and the normal level of
XX expression of the marker in a control non-breast cancer sample, where a
XX significant increase in the level of expression of the marker in the
XX patient sample and the normal level is an indication that the patient is
XX afflicted with breast cancer. The breast cancer associated sequences from
XX the present invention have cytostatic activities and can be used in gene
XX therapy. The method is useful for diagnosing and treating breast cancer.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 247 AA;
XX
Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123; Indels 0; Gaps 0;
Matches 247; Conservative 0; Mismatches 0;
QY 1 MLQNSAVLLVLVISATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFFVKESLKCANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFFVKESLKCANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPETAITEVQLPNHFNSRNYNRLVRSLLCEDETVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAITEVQLPNHFNSRNYNRLVRSLLCEDETVSTIRD 180
QY 181 SLMEKIGPNWASLFHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNWASLFHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
RESULT 11
ABG72290
ID ABG72290 standard; protein; 247 AA.

XX	ABG72290;	Db	121	IAEVQECYSKLVCSIAKRNPEAITEVQVLPNHFSNRYNRLVRSILLECDEDTVTIRD	180
AC					
XX		Qy	181	SIMKEIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK	240
XX	14-MAR-2003 (first entry)	Db	181	SIMKEIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK	240
XX	Human Corpuscles of Stannius protein.	Qy	241	RTSHESA 247	
XX	Human; Corpuscles of Stannius protein; calcium uptake inhibitor;	Db	241	RTSHESA 247	
KW	renal excretion of phosphate; electrolyte disorder; renal disease;				
KW	bone disease; heart disease; arterial hypertension; bone resorption;				
KW	osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;				
KW	hypervitaminosis D; tumour; serum calcium level; sarcoidosis;				
KW	hyperthyroidism; adrenal insufficiency; serum albumin; plasma protein;				
KW	GI calcium absorption; stannioalcalin; osteopathic; cytostatic;				
KW	hypotensive.				
XX					
OS	Homo sapiens.				
XX					
XX	US2002146791-A1.				
PN					
XX	10-OCT-2002.				
PD					
XX	05-APR-2002; 2002US-00116051.				
XX					
PF					
XX	08-MAR-1994; 94US-00208005.				
PR					
PR	28-APR-1995; 95US-00431117.				
PR	17-MAY-1999; 99US-00312610.				
XX					
XX	(HUMA-) HUMAN GENOME SCI INC.				
PA					
XX					
XX	Olsen HS, Adams MD;				
PI					
XX	WPI; 2003-147579/14.				
DR	N-PSDB; ABX15152.				
XX					
XX	Isolated polynucleotide for encoding polypeptides used to diagnose and				
PT	treat electrolyte disorders leading to renal disease, e.g. Paget's				
PT	disease, hypercalcaemia and sarcoidosis.				
XX					
XX	Claim 13; Fig 1; 26pp; English.				
PS					
XX	The present invention relates to the isolation of human Corpuscles of				
CC	Stannius protein, and the polynucleotide sequence encoding it. Human				
CC	Corpuscles of Stannius protein inhibits calcium uptake and reduces renal				
CC	excretion of phosphate. The polynucleotide sequence is useful for				
CC	encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in				
CC	the treatment of electrolyte disorders that lead to renal, bone or heart				
CC	disease, such as arterial hypertension, disorders due to elevated bone				
CC	resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia				
CC	(e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum				
CC	calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal				
CC	insufficiency, loss of serum albumin secondary to renal diseases, or				
CC	excessive GI calcium absorption and elevated concentration of plasma				
CC	proteins. The encoded polypeptide exhibits a high degree of homology to				
CC	Stannioalcalin from Anguilla australis and from Oncorhynchus kisutch. The				
CC	present sequence represents human corpuscles of stannius protein				
XX					
XX	Sequence 247 AA;				
SQ					
	Query Match 100.0%; Score 1268; DB 6; Length 247;				
	Best Local Similarity 100.0%; Pred. No. 1.1e-123;				
	Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 MLQNSAVLLVLVTSASATHEAQNDVSVPKRSVAAQNSAEVVRCLNSALQVCGAFACL	60			
Db	1 MLQNSAVLLVLVTSASATHEAQNDVSVPKRSVAAQNSAEVVRCLNSALQVCGAFACL	60			
Qy	61 ENSTCTDGYDICKSFLYSAAKFDGKAFVKESLKIANGVTSKVFLAIRCSTFORM	120			
Db	61 ENSTCTDGYDICKSFLYSAAKFDGKAFVKESLKIANGVTSKVFLAIRCSTFORM	120			
Qy	121 IAEVQECYSKLVCSIAKRNPEAITEVQVLPNHFSNRYNRLVRSILLECDEDTVTIRD	180			

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFYSAKFTQKAFVKESLKCANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTDMYDICKSFYSAKFTQKAFVKESLKCANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTVTRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTVTRD 180
QY 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
Db 241 RTSHEA 247

RESULT 13
ADI30575
ID ADI30575 standard; protein; 247 AA.
XX
AC ADI30575;
XX
DT 22-APR-2004 (first entry)
XX
DE Human stannioalcalcin protein.
XX
KW human; stannioalcalcin-alpha; electrolyte imbalance; hypertension;
KW hyperglycaemia; migraine; renal disease; heart disease; bone disease;
KW osteoporosis; hypoglycaemia; Paget's disease.
XX
OS Homo sapiens.
XX
PN US2003181663-A1.
XX
PD 25-SEP-2003.
XX
PF 18-APR-2003; 2003US-00418226.
XX
PR 10-NOV-1994; 94WO-US013206.
PR 02-JUN-1995; 95US-00460529.
PR 28-JUL-1999; 99US-00361736.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Olsen HS, Fleischmann RD;
XX
XX WPI; 2003-852260/79.
XX
XX New human stannioalcalcin-alpha polypeptide, useful in regulating
PT electrolyte imbalances, or for diagnosing and treating a disease
PT associated with mutated forms of stannioalcalcin-alpha sequences, e.g.
PT renal disease or osteoporosis.
XX
XX Disclosure; SEQ ID NO 10; 22pp; English.
XX

CC The invention comprises the amino acid and coding sequence of a human
CC stannioalcalcin-alpha protein. The DNA and protein sequences of the
CC invention are useful for regulating electrolyte imbalances to treat
CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences
CC are also useful in diagnosing and treating a disease associated with
CC mutated forms of stannioalcalcin-alpha sequences, such as: renal disease,
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The
CC present amino acid sequence represents a human stannioalcalcin protein.
XX

SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFYSAKFTQKAFVKESLKCANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTDMYDICKSFYSAKFTQKAFVKESLKCANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTVTRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPETAEVTVVQLPNHFSNRYNRLVRSLLCEDTSTVTRD 180
QY 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
Db 241 RTSHEA 247

RESULT 14
AB084399
ID AB084399 standard; protein; 247 AA.
XX
AC AB084399;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stannioalcalcin protein.
XX
KW Human; antitense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX N-PSDB; ABD20997.

XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCTIANGVTSKVFLAIRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCTIANGVTSKVFLAIRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRTTNEPQKLVLLRNLRGEBEDSPSHIK 240
DB 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRTTNEPQKLVLLRNLRGEBEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 15
ADQ21382
ID ADQ21382 standard; protein; 247 AA.
XX
AC ADQ21382;
XX
DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 4202.
DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
KW Homo sapiens.
OS
XX WO2004048938-A2.
FN
XX 10-JUN-2004.
PD
XX 26-NOV-2003; 2003WO-US038193.
PF
XX 26-NOV-2002; 2002US-0429739P.
PR
XX (PROT-) PROTEIN DESIGN LABS INC.
PA
XX Aziz N, Ginsburg WM, Zlotnik A;
PI WPI; 2004-441208/41.
XX
DR Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 4202; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

Query Match 100.0%; Score 1268; DB 8; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
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DB 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCTIANGVTSKVFLAIRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRTTNEPQKLVLLRNLRGEBEDSPSHIK 240
DB 181 SLMEKIGPNMASLFILQTDHCAQTHPRADFNRRTTNEPQKLVLLRNLRGEBEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

Search completed: April 4, 2006, 14:10:41
Job time : 193 secs

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OM protein - protein search, using sw model

Run on: April 4, 2006, 14:14:54 ; Search time 47 Seconds
(without alignments)
434.487 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	1	US-08-208-005C-2
2	1268	100.0	247	1	US-09-038-597A-2
3	1268	100.0	247	1	US-08-460-529B-10
4	1268	100.0	247	1	US-08-431-117A-2
5	1268	100.0	247	2	US-09-361-736B-10
6	1268	100.0	247	2	US-09-949-016-6319
7	1268	100.0	247	2	US-09-787-397A-4
8	1268	100.0	247	2	US-09-705-500A-3
9	1268	100.0	247	2	US-10-418-226-10
10	1268	100.0	341	2	US-09-949-016-11426
11	660.5	52.1	204	1	US-08-208-005C-5
12	660.5	52.1	204	1	US-09-038-597A-5
13	628	49.5	170	1	US-08-460-529B-9
14	628	49.5	170	2	US-09-361-736B-9
15	628	49.5	170	2	US-10-418-226-9
16	354.5	28.0	296	2	US-08-831-132-14
17	354.5	28.0	296	2	US-09-416-150-14
18	354	27.9	302	2	US-08-831-132-2
19	354	27.9	302	2	US-09-416-150-2
20	354	27.9	302	2	US-09-193-881-23
21	354	27.9	302	2	US-09-361-736B-12
22	354	27.9	302	2	US-10-418-226-12
23	354	27.9	346	2	US-09-949-016-10679
24	351.5	27.7	251	2	US-09-361-736B-2
25	351.5	27.7	251	2	US-10-418-226-2
26	333.5	26.3	251	1	US-08-460-529B-2
27	91	7.2	901	2	US-09-828-062-8

28	90	7.1	281	2	US-09-973-278-172	Sequence 172, App
29	90	7.1	281	2	US-09-973-278-277	Sequence 277, App
30	89.5	7.1	10182	2	US-09-134-001C-3159	Sequence 3159, App
31	86	6.8	500	2	US-09-198-452A-299	Sequence 299, App
32	86	6.8	500	2	US-09-438-185A-288	Sequence 288, App
33	85.5	6.7	311	2	US-09-710-279-2460	Sequence 2460, App
34	85.5	6.7	656	2	US-09-134-001C-4322	Sequence 4322, App
35	83.5	6.6	290	2	US-09-655-908-6	Sequence 6, Appli
36	83.5	6.6	290	2	US-09-655-908-8	Sequence 8, Appli
37	83.5	6.6	1027	2	US-09-762-724-8	Sequence 8, Appli
38	83.5	6.6	1029	2	US-09-762-724-6	Sequence 792, App
39	83	6.5	319	2	US-09-710-279-792	Sequence 2008, App
40	83	6.5	319	2	US-09-710-279-2008	Sequence 44, Appli
41	83	6.5	398	2	US-09-710-279-44	Sequence 1498, App
42	83	6.5	398	2	US-09-710-279-1498	Sequence 3810, App
43	82	6.5	417	2	US-09-134-001C-3810	Sequence 4670, App
44	82	6.5	362	2	US-09-134-001C-4670	Sequence 4, Appli
45	81	6.4	680	2	US-09-298-924-4	

ALIGNMENTS

RESULT 1
US-08-208-005C-2
; Sequence 2, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpules of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-2

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAFQNDVSFPRKSRVAQNSAEVVRCLNSALQVCGGAFACL 60
|||||

Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAPACL 60
Qy 61 ENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
Qy 121 IAEVQEECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLLECEDTSTIRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLLECEDTSTIRD 180
Qy 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLNRLNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLNRLNLRGEEDSPSHIK 240
Qy 241 RTSHEA 247
Db 241 RTSHEA 247

RESULT 2

US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stannioalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
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Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLNRLNLRGEEDSPSHIK 240
Qy 241 RTSHEA 247
Db 241 RTSHEA 247

RESULT 3

US-08-460-529B-10
; Sequence 10, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stannioalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-460-529B-10

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAPACL 60
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Db 61 ENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
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Db 181 SLMEKIGPNMASLFILOTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 4

US-08-431-117A-2
; Sequence 2, Application US/08431117A
; Patent No. 5954301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
Db 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCTDGMVDICKSFYLSAAKFTDQKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCTDGMVDICKSFYLSAAKFTDQKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYKLVNCSIAKRNPFAITVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
Db 121 IAEVQECYKLVNCSIAKRNPFAITVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
QY 181 SLMEKIGPNMASLFILOTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLFILOTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 5

US-09-361-736B-10
; Sequence 10, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143PLD1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
Db 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCTDGMVDICKSFYLSAAKFTDQKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCTDGMVDICKSFYLSAAKFTDQKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYKLVNCSIAKRNPFAITVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
Db 121 IAEVQECYKLVNCSIAKRNPFAITVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
QY 181 SLMEKIGPNMASLFILOTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFILOTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 6

US-09-949-016-6319
; Sequence 6319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

103 PRIOR FILING DATE: 1995-06-02
104 PRIOR APPLICATION NUMBER: PCT/US94/13206
105 PRIOR FILING DATE: 1994-11-30
106 NUMBER OF SEQ ID NOS: 12
107 SOFTWARE: Patent in version 3.1
108 SEQ ID NO 10
109 TYPE: PRT
110 ORGANISM: human
111 US-01418-226-10

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLSASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVLSASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
QY 181 SLMEKIGPNMASLFHILOTHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFHILOTHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 10
US-09-949-016-11426
Sequence 11426, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11426
LENGTH: 341
TYPE: PRT
ORGANISM: Human
US-09-949-016-11426

Query Match 100.0%; Score 1268; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 4.3e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLSASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 95 MLQNSAVLLVLSASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 154
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKIANGVTSKVFLAIRRCSTFORM 120
DB 155 ENSTCDTDMYDICKSFLYSAAKFDTGKAFVKESLKIANGVTSKVFLAIRRCSTFORM 214

QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 180
DB 215 IAEVQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRD 274
QY 181 SLMEKIGPNMASLFHILOTHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 275 SLMEKIGPNMASLFHILOTHCAQTHPRADFNRRTNEPQKLVLLRNLRGEEDSPSHIK 334
QY 241 RTSHESA 247
DB 335 RTSHESA 341

RESULT 11
US-08-208-005C-5
Sequence 5, Application US/08208005C
Patent No. 5837498
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Coruscules of Stannius Protein, Stanniocalcin
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,005C
FILING DATE: 8 MARCH 1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCES/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Query Match 52.1%; Score 660.5; DB 1; Length 204;
Best Local Similarity 60.8%; Pred. No. 4.9e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

QY 11 LVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDM 70
DB 12 LVIGTAATDTPDEA-SPPRARFSSNSPDSVARCLNGALAVCGGTFACLENSTCDTDM 70
QY 71 YDICKSFLYSAAKFDTGKAFVKESLKIANGVTSKVFLAIRRCSTFORMIAEVQECYS 130
DB 71 HDICQLFHTAATFNTQGTQKTFVKESLKIANGVTSKVFTIRRCGVFORMISEVQECYS 130
QY 131 KLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVTSTIRDSLMKIGPNM 190
DB 131 RLDICGVARSNPEAIGEVVQVPAHFENRYSTLLQSLACDEBTAVVAVRAGLVARLGPDM 190

QY 191 ASLPHILOTDHCAQ 204
DB 191 ETLFQLLNKHCPQ 204

RESULT 12

US-09-038-597A-5
; Sequence 5, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-09-038-597A-5

Query Match 52.1%; Score 660.5; DB 1; Length 204;
Best Local Similarity 60.8%; Pred. No. 4.9e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

QY 11 LVTSASATHEAQNDSVPSKSRVAQNSAEVVRCLNSALQVCGGAFACLENSTCDTGM 70
DB 12 LVLGTAATFTDPEEA-SPRRARFSSNSPSDVARCLNGALAVCGTFAACLENSTCDTGM 70
QY 71 YDICKSFLYSAAKFDQKAFVKESLKCANGVTSKVFLAIRRCSSTFORMIAEVEQECYS 130
DB 71 HDICQLFFHTANTFTQKTFVKESLRCIANGVTSKVFTIRRCGVFORMISEVEQECYS 130
QY 131 KLVNCSIAKENPAITEVQQLPHNFSNRYNRLVRSLLCEDTSTVTRDSLMKEKIGPNM 190
DB 131 RLDCIGVARSNPEAIGEVQVPAHFPPNRYSTLLQSLACDEBTAVVVRAGLVARLGPDM 190
QY 191 ASLPHILOTDHCAQ 204
DB 191 ETLFQLLNKHCPQ 204

RESULT 13

US-08-460-529B-9

; Sequence 9, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-460-529B-9
Query Match 49.5%; Score 628; DB 1; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.9e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;
QY 28 SPRKSRVAQNSAEVVRCLNSALQVCGGAFACLENSTCDTGM YDICKSFLYSAAKFDQ 87
DB 1 SPRTARFSSASSPSDVARCLNGALQVCGSFAACLDNSTCNTDGMHEICRSFLHGA AKFDQ 60
QY 88 GKAFVKESLKCANGVTSKVFLAIRRCSSTFORMIAEVEQECYSKLVNCSIAKENPAITE 147
DB 61 GKTFFVKESLKCANGITTSKVTIRRCSSFSQKMISEVQECYSKLDLCSVAQSNPEAMGE 120
QY 148 VVQLPHNFSNRYNRLVRSLLCEDTSTVTRDSLMKEKIGPNMASLPHIL 197
DB 121 VAQVSPQFPNRYSTLLQSLTCDDETVQVRAGLVSRLEPEMGVLFQLL 170
RESULT 14
US-09-361-736B-9
; Sequence 9, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-09-361-736B-9

Query Match 49.5%; Score 628; DB 2; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.9e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 28 SPRKSRVAQNSAEVVRCLNSALQVCGAFACLENSTCDTDGMYDICKSFLYSAAKFDQ 87
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |
Db 1 SPTAFPSASSPSDVARCLNGALQVCGSAFACLDNSTONTDGMHEICRSFLHGAAKFDQ 60
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |

QY 88 GKAFVKESLKCITANGVTSKVFLAIRRCSTFORMIAEVQECYSKLVNCSIAKNPEAITE 147
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |
Db 61 GKTFFVKESLKCITANGITSKVFLTIRRCSSFQKMISEVQECYSKLDLCSVAQSNPEAMGE 120
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |

QY 148 VVOLPNHFSNRYNRLVRSLLCEDTDTVSTIRDSLMKEIGPNNASLPHIL 197
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |
Db 121 VAQVPSQFPNRYYSTLLQSLTCDTVEQVRAGLVSRLEPEMVGVLQQL 170
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |

RESULT 15
US-10-418-226-9
; Sequence 9, Application US/10418226
; Patent No. 6955885
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143PID2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-10-418-226-9

Query Match 49.5%; Score 628; DB 2; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.9e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 28 SPRKSRVAQNSAEVVRCLNSALQVCGAFACLENSTCDTDGMYDICKSFLYSAAKFDQ 87
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |
Db 1 SPTAFPSASSPSDVARCLNGALQVCGSAFACLDNSTONTDGMHEICRSFLHGAAKFDQ 60
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |

QY 88 GKAFVKESLKCITANGVTSKVFLAIRRCSTFORMIAEVQECYSKLVNCSIAKNPEAITE 147
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |
Db 61 GKTFFVKESLKCITANGITSKVFLTIRRCSSFQKMISEVQECYSKLDLCSVAQSNPEAMGE 120
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |

QY 148 VVOLPNHFSNRYNRLVRSLLCEDTDTVSTIRDSLMKEIGPNNASLPHIL 197
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |
Db 121 VAQVPSQFPNRYYSTLLQSLTCDTVEQVRAGLVSRLEPEMVGVLQQL 170
| | | : : : : : | | | : : : : : | | | : : : : : | | | : : : : : |

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2006, 14:07:39 ; Search time 231 Seconds
(without alignments)
754.396 Million cell updates/sec

Title: US-09-703-350B-76

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	1 STC1 HUMAN	P52823 homo sapien
2	1234	97.3	247	1 STC1_MOUSE	O55183 mus musculus
3	1231	97.1	247	1 STC1_RAT	F97574 rattus norv
4	1228	96.8	247	2 Q71UE3_MOUSE	Q71ue3 mus musculus
5	1199	94.6	247	1 STC1_BOVIN	Q9n0t1 bos taurus
6	1192.5	94.0	246	2 Q7TSN9_MOUSE	Q7tsn9 mus musculus
7	873	68.8	251	2 O5XGL3_XENLA	O5xgl3 xenopus lae
8	851	67.1	253	2 Q6DFI8_XENLA	Q6dfi8 xenopus lae
9	797	62.9	157	2 Q71UE5_HUMAN	Q71ue5 homo sapien
10	779.5	61.5	252	2 Q800I4_LEPOS	Q800i4 lepisosteus
11	778.5	61.4	252	2 Q800I5_AMICA	Q800i5 amia calva
12	682	53.8	250	1 STC ANGAU	P18301 anguilla au
13	662.5	52.2	256	1 STC_ONCKI	Q08264 oncorhynch
14	662.5	52.2	256	1 STC_ONCMY	Q43648 oncorhynch
15	660	52.1	249	2 Q4RIC1_CATCO	Q4ric1 catostomus
16	654	51.6	249	2 Q98TB7_9TELE	Q98tb7 osteoglossu
17	653	51.5	249	2 Q6NYL8_BRARE	Q6nyl8 brachydanio
18	653	51.5	249	2 Q6PHV3_BRARE	Q6phv3 brachydanio
19	649	51.2	249	2 Q51RA8_BRARE	Q51ra8 brachydanio
20	634	50.0	249	2 Q4RIC3_9TELE	Q4ric3 gnathonemus
21	626.5	49.4	251	2 Q4RIC2_PANBU	Q4ric2 pantodon bu
22	617	48.7	179	1 STC_ONCKS	P43647 oncorhynch
23	603.5	47.6	251	2 Q5SBH7_PLAFE	Q5sbh7 platichthys
24	593	46.8	254	2 Q5IRB0_FUGRU	Q5irb0 fugu rubrip
25	583	46.0	255	2 Q4RIC0_PERO	Q4ric0 micropterus
26	572	45.1	204	2 Q4SLS9_TETNG	Q4sls9 tetraodon n
27	425	33.5	119	2 Q4RCR1_TETNG	Q4rcr1 tetraodon n
28	371	29.3	294	2 Q4RN85_TETNG	Q4rn85 tetraodon n
29	361.5	28.5	283	2 Q51RA9_FUGRU	Q51ra9 fugu rubrip
30	356	28.1	283	2 Q51RA7_BRARE	Q51ra7 brachydanio
31	354.5	28.0	296	1 STC2_MOUSE	O88452 mus musculus

32	354.5	28.0	296	2 Q9DCS6_MOUSE	Q9dcs6 mus musculus
33	354.5	28.0	296	2 Q5SS12_MOUSE	Q5ss12 mus musculus
34	354	27.9	302	1 STC2_HUMAN	O76061 homo sapien
35	354	27.9	302	2 Q6PHC9_HUMAN	Q6phc9 homo sapien
36	352	27.8	302	1 STC2_MACNE	O97561 macaca neme
37	349	27.5	296	1 STC2_RAT	O9r0k8 rattus norv
38	340	26.8	302	1 STC2_PONPY	Q5rat2 pongo pygma
39	295.5	23.3	198	2 Q4RRX5_TETNG	Q4rrx5 tetraodon n
40	181.5	14.3	197	1 STC2_CAVPO	P57675 cavia porce
41	156	12.3	40	1 STC_ONCNE	P43649 oncorhynch
42	104.5	8.2	1207	2 Q4UBC6_THEAN	Q4ubc6 theileria a
43	104	8.2	1044	2 Q7QT48_GIALA	Q7qt48 giardia lam
44	102	8.0	473	2 Q9S216_ARATH	Q9s216 arabidopsis
45	99	7.8	1001	2 Q5CUF1_CRYPV	Q5cuf1 cryptospori

ALIGNMENTS

RESULT 1
STC1_HUMAN STANDARD; PRT; 247 AA.
AC F52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Stanniocalcin-1 precursor (STC-1).
GN Name-STC1; Synonyms-STC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Fibrosarcoma, and Lung carcinoma;
RX MEDLINE=96077825; PubMed=7489828; DOI=10.1016/0303-7207(95)03601-3;
RA Chang A.C.-M., Janosi J., Hulsbeek M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone stanniocalcin.";
RL Mol. Cell. Endocrinol. 112:241-247 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Retal lung;
RX MEDLINE=96312491; PubMed=8700837; DOI=10.1073/pnas.93.5.1792;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stanniocalcin: a possible hormonal regulator of mineral metabolism.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX Jeffrey K.J., Reddel R.R.;
RT "Characterization of the human stanniocalcin 1 gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon, Kidney, and Stomach;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zensberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy M., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PROTEIN SEQUENCE OF 19-32.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites";
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC therefore prevent hypercalcaemia.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in most tissues, with the highest
CC levels in ovary, prostate, heart, kidney and thyroid. In the
CC kidney, expression is confined to the nephron, specifically in the
CC distal convoluted tubule and in the collecting tubule. Not
CC detected in the brain, liver, spleen, peripheral blood leukocytes
CC and adrenal medulla.
CC -!- SIMILARITY: Belongs to the stannocalcin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U25997; AAC09472.1; -; mRNA.
CC EMBL; U46768; AAA88903.1; -; mRNA.
CC EMBL; AF242179; AAL79522.1; -; Genomic_DNA.
CC EMBL; BC029044; AAB29044.1; -; mRNA.
CC ENSEMBL; ENSG00000159167; Homo sapiens.
CC HGNC; HGNC:11373; STCL.
CC H-InvDB; HIX0007390; -.
CC MIM; 601185; -.
CC GO; GO:0005179; F: hormone activity; TAS.
CC GO; GO:0006874; P: calcium ion homeostasis; TAS.
CC GO; GO:0007466; P: cell surface receptor linked signal transdu. . .; TAS.
CC GO; GO:0007467; P: cell-cell signaling; TAS.
CC GO; GO:0007584; P: response to nutrients; TAS.
CC InterPro; IPR004978; Stannocalcin.
CC PANTHER; PTHR11245; Stannocalcin.
CC Pfam; PF03298; Stannocalcin.
KW Direct protein sequencing; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 17
FT PROPEP 18 33 Potential.
FT CHAIN 34 247 Stannocalcin-1.
FT CARBOHYD 62 62 N-linked (GlcNAc . . .) (Potential).
FT DISULFID 45 59 By similarity.
FT DISULFID 54 74 By similarity.
FT DISULFID 65 114 By similarity.
FT DISULFID 98 128 By similarity.
FT DISULFID 135 170 By similarity.
FT DISULFID 202 202 Interchain (By similarity).
SQ SEQUENCE 247 AA; 27621 MW; 1E4A8BDB61B49AED CRC64;

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLTVSATNTHAEQNDVSVPKRSVAAQNSAEVVRCNLNSALQVCGGAFACL 60
DB |||||
QY 1 MLQNSAVLLVLTVSATNTHAEQNDVSVPKRSVAAQNSAEVVRCNLNSALQVCGGAFACL 60
DB |||||
QY 61 ENSTCTDGTGMYDICKSPLYSAAKFDYTGKAFVKESLKIANGVTSTKVFLLAIRCSTFORM 120
DB 61 ENSTCTDGTGMYDICKSPLYSAAKFDYTGKAFVKESLKIANGVTSTKVFLLAIRCSTFORM 120

QY 121 IAEVOECYSKLVNCSIAKRNPFAITVVQLPNHFNSRYNRLVRSLLCEDEDTVTSTIRD 180
DB |||||
QY 121 IAEVOECYSKLVNCSIAKRNPFAITVVQLPNHFNSRYNRLVRSLLCEDEDTVTSTIRD 180
DB |||||
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNBPQKVKVLLRNLRGDEDSPSHIK 240
DB |||||
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNBPQKVKVLLRNLRGDEDSPSHIK 240
DB |||||
QY 241 RTSHESA 247
DB |||||
QY 241 RTSHESA 247
DB |||||
RESULT 2
STCL_MOUSE STANDARD; PRT; 247 AA.
ID STCL_MOUSE
AC O55183;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Stannocalcin-1 precursor (STC-1).
GN Name=Stcl; Synonyms=Stc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=BALB/c;
RX MEDLINE=97179050; PubMed=9027337; DOI=10.1016/S0303-7207(96)03929-9;
RA Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;
RT "Molecular cloning and characterization of mouse stannocalcin cDNA.";
RL Mol. Cell. Endocrinol. 124:185-187(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC therefore prevent hypercalcaemia (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC -!- SIMILARITY: Belongs to the stannocalcin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U47815; AAC00050.1; -; Genomic DNA.
CC EMBL; BC021425; AAB21425.1; -; mRNA.
CC ENSEMBL; ENSMUSG00000014813; Mus musculus.

DR MGI:109131; Stcl.
DR GO:0005615; C:extracellular space; IDA.
DR GO:0005179; F:hormone activity; TAS.
DR GO:0006874; P:calcium ion homeostasis; TAS.
DR GO:0003020; P:monovalent inorganic anion homeostasis; TAS.
DR InterPro: IPR004978; Stanniocalcin.
DR PANTHER: PTHR11245; Stanniocalcin; 1.
DR Pfam: PF03298; Stanniocalcin; 1.
KW Glycoprotein; Hormone; Signal.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 33 Potential.
FT CHAIN 34 247 Stanniocalcin-1.
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
FT DISULFID 45 59 By similarity.
FT DISULFID 54 74 By similarity.
FT DISULFID 65 114 By similarity.
FT DISULFID 98 128 By similarity.
FT DISULFID 135 170 By similarity.
FT DISULFID 202 202 Interchain (By similarity).
SQ SEQUENCE 247 AA; 27480 MW; DAD30D08575A513B CRC64;

Query Match 97.3%; Score 1234; DB 1; Length 247;
Best Local Similarity 96.4%; Pred. No. 8.9e-97;
Matches 238; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLQNSAVLVVISATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVILALVISAAAAHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFAVKESLKIANGVTSKVFLAIRRCSFTFQRM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFAVKESLKIANGVTSKVFLAIRRCSFTFQRM 120

QY 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQLPNHFNSRYYNRLVRSLLCEDETVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQLPNHFNSRYYNRLVRSLLCEDETVSTIRD 180

QY 181 SLMEKIGPNNASLFIHQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNNASLFIHQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240

QY 241 RTSQENA 247
DB 241 RTSQENA 247

RESULT 3
STCL_RAT STANDARD; PRT; 247 AA.
AC P97574;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Stanniocalcin-1 precursor (STC-1).
GN Name=Stcl; Synonym=Stc;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [RNA].
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could therefore prevent hypercalcemia (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL: U62667; AAB39541.1; -; mRNA.
DR EMBL: BC078803; AAB78803.1; -; mRNA.
DR Ensembl: ENSRNOG00000015075; Rattus norvegicus.
DR RGD: 621776; Stcl.
DR GO:0006874; P:calcium ion homeostasis; TAS.
DR GO:0001503; P:ossification; IDA.
DR InterPro: IPR004978; Stanniocalcin.
DR PANTHER: PTHR11245; Stanniocalcin; 1.
DR Pfam: PF03298; Stanniocalcin; 1.
KW Glycoprotein; Hormone; Signal.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 33 Potential.
FT CHAIN 34 247 Stanniocalcin-1.
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
FT DISULFID 45 59 By similarity.
FT DISULFID 54 74 By similarity.
FT DISULFID 65 114 By similarity.
FT DISULFID 98 128 By similarity.
FT DISULFID 135 170 By similarity.
FT DISULFID 202 202 Interchain (By similarity).
SQ SEQUENCE 247 AA; 27507 MW; DAC2FD08575A513B CRC64;

Query Match 97.1%; Score 1231; DB 1; Length 247;
Best Local Similarity 96.0%; Pred. No. 1.6e-96;
Matches 237; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLQNSAVLVVISATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVILALVISAAAAHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFAVKESLKIANGVTSKVFLAIRRCSFTFQRM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGAFAVKESLKIANGVTSKVFLAIRRCSFTFQRM 120

QY 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQLPNHFNSRYYNRLVRSLLCEDETVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPETAEVTVQLPNHFNSRYYNRLVRSLLCEDETVSTIRD 180

QY 181 SLMEKIGPNNASLFIHQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNNASLFIHQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240

QY 241 RTSQENA 247
DB 241 RTSQENA 247

RESULT 4
Q71UE3_MOUSE PRELIMINARY; PRT; 247 AA.
ID Q71UE3_MOUSE PRELIMINARY;
AC Q71UE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stanniocalcin.
GN Name=Stcl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., DiMattia G.E.;

```
RT "Comparative Analysis of Mammalian Stanniocalcin Genes.";
RL Endocrinology 139:4717-4725(1998).
DR EMBL; AF099098; AAC72394.1; -; mRNA.
DR MGI; MGI:109131; Stc1.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005179; F:hormone activity; TAS.
DR GO; GO:0008874; P:calcium ion homeostasis; TAS.
DR GO; GO:0003020; P:monovalent inorganic anion homeostasis; TAS.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
DR SEQUENCE 247 AA; 27495 MW; CA2DEDE659BAAF6B CRC64;
SQ
Query Match 96.8%; Score 1228; DB 2; Length 247;
Best Local Similarity 96.0%; Pred. No. 2.9e-96;
Matches 237; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 MLQNSAVILVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFCL 60
DB 1 MLQNSAVILALVISAAAHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFCL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCICANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQVLPNHFNSRYYNRLVRSLLCEDDVTSTIRD 180
DB 121 IAEVQEDCYSKLVNCSIAKRNPEAITEVQVLPNHFNSRYYNRLVRSLLCEDDVTSTIRD 180
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGDESPSHIK 240
DB 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGDESPSHIK 240
QY 241 RTSQESA 247
DB 241 RTSQESA 247
RESULT 5
STCL_BOVIN STANDARD; PRT; 247 AA.
AC Q9N0T1;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Stanniocalcin-1 precursor (STC-1).
GN Name=STC1; Synonyms=STC;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ovary;
RA DiMattia G.E.;
RT "Bovine stanniocalcin cDNA sequence.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates renal phosphate reabsorption, and could
CC therefore prevent hypercalcemia (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SIMILILARITY: LOCATTON: Secreted (By similarity).
CC -!- SUBCELLULAR: Belongs to the stanniocalcin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ENBL; AF257506; AAP68996.1; -; mRNA.
DR InterPro; IPR004978; Stanniocalcin.
DR
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DR PANTHER; PTHR11245; Stanniocalcin; 1.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Glycoprotein; Hormone; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 247 Stanniocalcin-1.
FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
FT DISULFID 45 59 By similarity.
FT DISULFID 54 74 By similarity.
FT DISULFID 65 114 By similarity.
FT DISULFID 98 128 By similarity.
FT DISULFID 135 170 By similarity.
FT DISULFID 202 202 Interchain (By similarity).
SQ SEQUENCE 247 AA; 27555 MW; F9942A715E2A3DE0 CRC64;
Query Match 94.6%; Score 1199; DB 1; Length 247;
Best Local Similarity 94.7%; Pred. No. 8.5e-94;
Matches 234; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 MLQNSAVILVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFCL 60
DB 1 MLQNSAVILVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFCL 60
QY 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCICANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFLYSAAKFTQGAFAVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQVLPNHFNSRYYNRLVRSLLCEDDVTSTIRD 180
DB 121 IAEVQECYTKLVNCSVAKRNPEAITEVQVLPNHFNSRYYNRLVRSLLCEDDVTSTIRD 180
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGDESPSHIK 240
DB 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGDESPSHIK 240
QY 241 RTSQESA 247
DB 241 RTSQESA 247
RESULT 6
Q7TSN9_MOUSE PRELIMINARY; PRT; 246 AA.
AC Q7TSN9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stanniocalcin 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RA Chang A.C., Cha J., Reddel R.R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF512563; AAP47156.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR SEQUENCE 246 AA; 27423 MW; 4101C37EB6D743B2 CRC64;
Query Match 94.0%; Score 1192.5; DB 2; Length 246;
Best Local Similarity 93.9%; Pred. No. 3e-93;
Matches 232; Conservative 7; Mismatches 7; Indels 1; Gaps 1;
QY 1 MLQNSAVILVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFCL 60
DB 1 MLQNSAVILALVISAAAHEAEQNDVSVPKSRVAAQNSAEVVRCLNSACRLAAG-FACL 59
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QY 61 ENSTCDDTGMVDICKSFLYSAAKFTQGKAFVKESLKCIANGVTSKVFLAIRCSTFORM 120
DB 60 ENSTCDDTGMVDICKSFLYSAAKFTQGKAFVKESLKCIANGVTSKVFLAIRCSTFORM 119
QY 121 IAEVQECYCKLVNCSIAKRNPEATEVTVQVLPNHFNSRYNRLVRSLLCEDDTVTSTIRD 180
DB 120 IAEVQECYCKLVNCSIAKRNPEATEVTVQVLPNHFNSRYNRLVRSLLCEDDTVTSTIRD 179
QY 181 SLMEKIGPNMASHFILOTHDCAQTHPRADFNRRTNEPQKLVLLRNLRGEGDSPSHIK 240
DB 180 SLMEKIGPNMASHFILOTHDCAQTHPRADFNRRTNEPQKLVLLRNLRGEGDSPSHIK 239
QY 241 RTSQESA 247
DB 240 RTSQESA 246

RESULT 7
ID Q5XGL3_XENLA PRELIMINARY; PRT; 251 AA.
AC Q5XGL3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE LOC495194 protein.
GN Names:LOC495194;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084424; AAF84424.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000719; Prot_kinase.

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DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF02298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
SQ SEQUENCE 251 AA; 27823 MW; C0C00D19FB700E19 CRC64;

Query Match 68.8%; Score 873; DB 2; Length 251;
Best Local Similarity 70.7%; Pred. No. 4.8e-66;
Matches 164; Conservative 38; Mismatches 26; Indels 4; Gaps 3;

QY 5 SAVLL--VLVISASA--THEAEQND--VSPRKSRVAQNSAEVVRCLNSALQVCGGAFACL 60
DB 5 TALLLLPVLLSVSAGSYDTPDNDSQLGGRKGLASHSSVEVVRCLNGALQVCGGAFACL 64
QY 61 ENSTCDDTGMVDICKSFLYSAAKFTQGKAFVKESLKCIANGVTSKVFLAIRCSTFORM 120
DB 65 ENSTCDDTGMVDICKAFLYSAAKFTQGKVFVKESLKCIANGITSKVFLSIRCSLQRM 124
QY 121 IAEVQECYCKLVNCSIAKRNPEATEVTVQVLPNHFNSRYNRLVRSLLCEDDTVTSTIRD 180
DB 125 ISEVQDCYTKLDICTVAQYNPAITEVTVQVLPNHFNSRYNRLVRSLLCEDDTVTSTIRD 184
QY 181 SLMEKIGPNMASHFILOTHDCAQTHPRADFNRRTNEPQKLVLLRNLRGE 232
DB 185 SLMEQIGPNLANLFVQLGDKCSQIQPRMDFNRKNIIEPQKLIYLRNLRGE 236

RESULT 8
Q5DF18_XENLA PRELIMINARY; PRT; 253 AA.
ID Q5DF18;
AC Q5DF18;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Stcl-prov protein.
GN Name=stcl-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391 (2002).

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DE Stanniocalcin precursor.
GN Name=STC;
OS Ania calva (Bowfin). Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amniotes; Amniota; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14697312; DOI=10.1016/j.ygcen.2003.09.019;
RA Amemiya Y., Youson J.H.;
RT "Primary structure of stanniocalcin in two basal Actinopterygii.";
RL Gen. Comp. Endocrinol. 135:250-257(2004).
DR EMBL: AB106622; BAC66163.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005179; F:hormone activity; IEA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR004978; Stanniocalcin.
DR Pfam: PF03298; Stanniocalcin; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 32 Potential.
FT CHAIN 33 252 Potential.
FT SEQUENCE 252 AA; 27868 MW; B9D9663610DF0B5D CRC64;
SQ
Query Match 61.4%; Score 778.5; DB 2; Length 252;
Best Local Similarity 69.8%; Pred. No. 5.3e-58;
Matches 141; Conservative 37; Mismatches 23; Indels 1; Gaps 1;
QY 1 MLQNSAVLLVVISASATHEAQNDVS PRKSRVAQAQNSAEVVRCLNSALQVCGGAPACL 60
DB 1 MLHKTGILLVLLTSA-YELQDNEFSRPRTRVSAHSSDVARCLNSALQVCGGAPACL 59
QY 61 ENSTCDTDMYDICKSKFLYSAKFDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 60 ENSTCDTDMYDICKSKFLYSAKFDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 119
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDTSTVIRD 180
DB 120 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDTSTVIRD 179
QY 181 SLMEKIGPNMASLPHILOTHDC 202
DB 180 NLVSRIGPENSMLFQILQSKPC 201
RESULT 12
STC_ANGAU STANDARD; PRT; 250 AA.
AC P18301;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)
DE (Hypocalcin) (Teleocalcin).
GN Name=STC;
OS Anguilla australis (Australian eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7940;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 33-57.
RX MEDLINE=8083961; PubMed=3319739; DOI=10.1016/0303-7207(87)90149-3;
RA Butkus A., Roche P.J., Fernley R.T., Haralambidis J., Penschow J.D.,
RA Ryan G.B., Trabair J.F., Tregear G.W., Coghlan J.P.;
RT "Purification and cloning of a corpuscles of Stannius protein from
RT Anguilla australis.";
RL Mol. Cell. Endocrinol. 54:123-133(1987).
RN [2]
RP SEQUENCE REVISION.
RA Roche P.J.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Its primary function is the prevention of hypercalcemia.

CC Upon release into the circulation, it lowers calcium transport by
CC the gills, thereby reducing its rate of influx from the
CC environment into the extracellular compartment. STC also
CC stimulates phosphate reabsorption by renal proximal tubules. The
CC consequence of this action is increased levels of plasma
CC phosphate, which combines with excess calcium and promotes its
CC disposal into bone and scales.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- TISSUE SPECIFICITY: Corpuscles of Stannius.
CC -!- SIMILARITY: Belongs to the stanniocalcin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: M36967; AB91483.1; -; mRNA.
CC PIR: A54648; A54648.
CC InterPro: IPR004978; Stanniocalcin.
CC PANTHER: PTHR11245; Stanniocalcin; 1.
CC Pfam: PF03298; Stanniocalcin; 1.
CC Direct protein sequencing; Glycoprotein; Hormone; Signal.
CC SIGNAL 1 17 Potential.
CC PROPEP 18 32 Potential.
CC CHAIN 33 250 Stanniocalcin.
CC CARBOHYD 61 61 N-linked (GlcNAc..) (Probable).
CC DISULFID 44 58 By similarity.
CC DISULFID 53 73 By similarity.
CC DISULFID 64 113 By similarity.
CC DISULFID 97 127 By similarity.
CC DISULFID 134 169 By similarity.
CC DISULFID 201 201 Interchain (By similarity).
CC SEQUENCE 250 AA; 27174 MW; BB972BD951F75B3E CRC64;
SQ
Query Match 53.8%; Score 682; DB 1; Length 250;
Best Local Similarity 54.3%; Pred. No. 8.6e-50;
Matches 138; Conservative 47; Mismatches 57; Indels 12; Gaps 6;
QY 1 MLQNSAVLLVVISASATHEAQNDVS PRKSRVAQAQNSAEVVRCLNSALQVCGGAPACL 60
DB 1 MLRMSGLILTLVL-VTAAYEQDESEPLSPRTARFSASPSDFVARCLNGALQVCGGAPACL 59
QY 61 ENSTCDTDMYDICKSKFLYSAKFDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
DB 60 DNSTCDTDMYDICKSKFLYSAKFDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 119
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDTSTVIRD 180
DB 120 IAEVQECYSKLVNCSIAKRNPEAITEVVLPHNFSNRYNRLVRSLLCEDTSTVIRD 179
QY 181 SLMEKIGPNMASLPHILOTHDC-----AQTHP-RADFNRRRTNEPQKLKVLNLRGEED 234
DB 180 GLVSRLEPEMGVLFQILQTHKACPPSAAGGTGPVGGGSRWPMGPPMFKI-QPNLRSRD- 237
QY 235 SPISHI--KRTSHES 246
DB 238 -PTHLFAKKRSTSS 250
RESULT 13
STC_ONCKI STANDARD; PRT; 256 AA.
ID STC_ONCKI
AC Q08264;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)
DE (Hypocalcin) (Teleocalcin).
GN Name=STC;
OS Oncorhynchus kisutch (Coho salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
CC

Db 71 HDICQLFFHTAATFNTQGTFFVKESLRCIANGVTSKVFTIRRCGVQFORMISEVQBECS 130
Qy 131 KLVNCSIAKRNPAITEVVLQPNHFSNRYNRLVRSLLCEDBDTSTIRDSLMKIGPNM 190
Db 131 RLIDICGVARSNEAIGEVVQVPAHPFNRYISTLLQLSLACDEETVAVVRAGLVARLGPDM 190
Qy 191 ASLFIHLQTDHCAQTHPRADFN-----RRRTNEPQKLKVLRLNLRGEEDESPSHI 239
Db 191 ETLLFQLLQNKHCPCQSGNSQGNAPAGWRWPMGSPSPSKI-QPSMRGRD--PTHL 241

RESULT 15
Q4R1C1 CATCO
ID Q4R1C1_CATCO PRELIMINARY; PRT; 249 AA.
AC Q4R1C1_2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Stanniocalcin precursor.
GN Name=STC;
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Corpuscle of Stannius;
RA Anemiyu Y., Marra L.E., Youson J.H.;
RT "primary structure of White sucker stanniocalcin."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB218776; BAD99602.1; -; mRNA.
KW Signal.
FT SIGNAL 1 31 Potential.
FT CHAIN 32 249 Potential.
SQ SEQUENCE 249 AA; 27673 MW; 6E1034172216D028 CRC64;

Query Match 52.1%; Score 660; DB 2; Length 249;
Best Local Similarity 59.9%; Pred. No. 6.4e-48;
Matches 121; Conservative 34; Mismatches 45; Indels 2; Gaps 2;

Qy 1 MLQNSAVLLVLVISASATHEAQNSVSPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
Db 1 MLKSGFLLFLVLTSA-YETNQ-DPAQPRARFSANSPDVARCLNGALQVCGATFACL 58

Qy 61 ENSTCDTDMYDICK3FLYSAAKFDTCGKAFVYESLKCIANGVTSKVFLAIRCSTFORM 120
Db 59 ENSTCDTDMYDICK3FLYSAAKFDTCGKAFVYESLKCIANGVTSKVFTIRRCSTFORM 118

Qy 121 IAEVQECYKLVNCSIAKRNPAITEVVLQPNHFSNRYNRLVRSLLCEDBDTSTIRDSLM 180
Db 119 IAEVQECYKLVNCSIAKRNPAITEVVLQPNHFSNRYNRLVRSLLCEDBDTSTIRDSLM 178

Qy 181 SLMEKIGPNMASLFIHLQTDHC 202
Db 179 GLVSRIGPDMVTLFQLLQNKPC 200

Search completed: April 4, 2006, 14:14:37
Job time : 233 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 4, 2006, 14:10:59 ; Search time 40 Seconds
(without alignments)
594.139 Million cell updates/sec

Title: US-09-703-350B-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	680.5	53.7	263	A54648	stanniocalcin prec
2	662.5	52.2	256	I51197	stanniocalcin - co
3	354	27.9	302	JE0357	stanniocalcin homo
4	150	11.8	40	B60841	teleocalcin - coho
5	149	11.8	40	A60841	teleocalcin - sock
6	123	9.7	33	S06337	teleocalcin - rain
7	102	8.0	473	T04799	hypothetical prote
8	94	7.4	1105	T18295	Ap-3 adaptor compl
9	90.5	7.1	289	T50776	hypothetical prote
10	90.5	7.1	783	T38690	probable regulator
11	89.5	7.1	1126	T01491	ubiquitin-protein
12	89	7.0	305	T08121	peroxidase (EC 1.1
13	88	6.9	473	T45354	hypothetical prote
14	87.5	6.9	1465	S45628	DNA-directed DNA p
15	86	6.8	470	T86526	Mg++ transporter
16	86	6.8	470	H72097	mg++ transporter
17	86	6.8	510	T45952	hypothetical prote
18	86	6.8	556	S51858	probable membrane
19	86	6.8	581	S58201	conserved hypothet
20	83	6.5	250	D69215	hypothetical prote
21	83	6.5	250	S30584	hypothetical prote
22	83	6.5	365	T06693	AP-3 complex beta3
23	83	6.5	1093	T50652	AP3-complex beta-3
24	83	6.5	1094	T50651	protein C4G2.2 [i
25	82.5	6.5	869	A88710	hypothetical prote
26	82.5	6.5	1483	S30015	hypothetical prote
27	82.5	6.5	1757	T05204	hypothetical prote
28	82.5	6.5	2335	T40186	probable phosphati
29	82.5	6.5	2535	T04824	hypothetical prote

ALIGNMENTS

RESULT 1

A54648
Stanniocalcin precursor - Australian eel
N:Alternate names: Stannius corpuscle secretory protein
C:Species: Anguilla australis (Australian eel)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: A54648
R:Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.;
Mol. Cell. Endocrinol. 54, 123-133, 1987
A:Title: Purification and cloning of a corpuscles of Stannius protein from Anguilla aus
A:Reference number: A54648; MUID:88083961; PMID:3319739
A:Accession: A54648
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-263 <BUT>
A:Cross-references: UNIPROT:P18301; UNIPARC:UPI000002BEB5
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-263/Product: stanniocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;
Best Local Similarity 61.4%; Pred. No. 2.3e-51;
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

QY 1 MLQNSAVLLVLVISATHEAQNDSPKRSVAAQNSAEVVRCLNSALQVCGAPACL 60
DB 1 MURMSGLIITLVL-VTAAYEQDESEPLSPRTARFSPASPSDVARCLNGALQVCSAFACL 59
QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTGKAFVKESLKCIANGVTSKVFLAIRCSTFORM 120
DB 60 DNSTCNTDGMHICRSFLHGAAKFDTGKTFVKESLKCIANGITSKVFLTIRCCSFQKM 119
QY 121 IAEVQECYSKLVNCSIAGNPEATEVVLQPHNSRYNRYNRLVRSLLCDEDTVSTIRD 180
DB 120 ISEVQECYSKLDLCSVAQNSPEANGVAQVSPFPNRYISTLLQLSLTCDDETVQVRA 179
QY 181 SLMEKIGPNMASLFILOTDHC 202
DB 180 GLVSRLEPENGVLQQLQKAC 201

RESULT 2

I51197
stanniocalcin - coho salmon
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51197
R:Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.
Mol. Cell. Endocrinol. 90, 7-15, 1992
A:Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.
A:Reference number: I51197; MUID:93246046; PMID:1363790
A:Accession: I51197
A>Status: preliminary; translated from GB/EMBL/DDBJ

Db 2 SSNSPDSVARCLNGALAVCGGTACLENSTCD 33

RESULT 7
T04799
hypothetical protein F10M23.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04799
R:Sevan, M.; Lecharny, A.; Chedford, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15385
A:Accession: T04799
A:Molecule type: DNA
A:Residues: 1-473 <REV>
A:Cross-references: UNIPROT:Q9SZ16; UNIPARC:UPI00000A64C3; EMBL:AL035440
A:Experimental source: cultivar Columbia; BAC clone F10M23
C:Genetics:
A:Map position: 4
A:Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3
A:Note: F10M23.100

Query Match 8.0%; Score 102; DB 2; Length 473;
Best Local Similarity 21.0%; Pred. No. 0.48;
Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

Qy 26 SVSPKSRVAAQNSAEVVRCLNSALQVCGGACLENSTCDT-----DGMVDICKSF-LYS 80
Db 50 NVYKKKVELAAKRAELQLTSD-----ATVELSNLTALGEKSYIDICDSNLSFP 100
Qy 81 AAKFDPTQGFVKESLKCIA-----NG-- 102
Db 101 LPDQKTSGT--IKEQSAIAPALEQLWQKEERVAFSDVQSQIKICEIAGGLNGPH 158
Qy 103 VTSKVLAIKRCSTFORMIAEVEECYSKL-----NVCSIAKRN-PEATEV-- 148
Db 159 VVDETDLKRLDDFKQLQELQKEKSDRLQKLVFEVSTVHDLCLDLFLSTVTEVHP 218
Qy 149 -----VQLPNHFSNRYNRLVRSLECEDTSTVIRSLMEKIGPNNASILFHILQT 199
Db 219 SLDEANGVQTS-IGNETLARIKTLVTLKEDQMKLKK--LQELATQUTDLNLMDT 273

RESULT 8
T18295
Ap-3 adaptor complex beta3A chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18295
R:Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rush
Hum. Mol. Genet. 8, 323-330, 1999
A:Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the m
A:Reference number: Z18864; MUID:99135912; PMID:9931340
A:Accession: T18295
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-1105 <FEN>
A:Cross-references: UNIPROT:Q9Z171; UNIPARC:UPI000002973F; EMBL:AF103809; NID:G3885987;
A:Experimental source: strain C3H/HeJ
C:Genetics:
A:Gene: Ap3b1
A:Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;
Best Local Similarity 21.2%; Pred. No. 6.5;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

Qy 1 MLQNSAVLLVIVISASATHEAQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGACFAC 60
Db 308 LQSRNAAVVMAVAQLYWH-----ISPKSE--AGVISKSLVRLLRNSREVOYIVLQNI 358
Qy 61 ENSTCDTDMYD-ICKSFLYSAAKFDQTQGFVKESLKCIANGVTSKVFL----- 109

Db 359 ATMSIERKGMFEPYKSPF-YVRSTDPTWIKTLKLEILTNLANEANISTLLREFFQYVRSQ 417
Qy 110 -----AIRRCSTFORMIAEVEECYSKLVCSIAKRNPEAITE---VVLQPNHFS 156
Db 418 DKQFAAATIQIGRCAT---SISFTETCFNGL-VCLLSNRDEIVVAESVWVVKLLQWQ 473
Qy 157 NRYNRLVRSLE-CDEDTSTVIRSLMEKIGPNNASILFHILQTDHCAQTHPRADFNRNR 215
Db 474 PAQGEIIRHAKFLDSITVPVARASILWIGEN-----CERVPKIA----- 515
Qy 216 TNEPQKLVLLRNLRGRED 234
Db 516 ---PDVLRKMAKSFSTSED 531

RESULT 9
T50776
hypothetical protein [imported] - Vitis vinifera
C:Species: Vitis vinifera
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50776
R:Matsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A:Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP protein:
A:Reference number: Z25233
A:Accession: T50776
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <MAT>
A:Cross-references: UNIPROT:P93798; UNIPARC:UPI0000135B10; EMBL:AB001375; PIDN:BAAL19246
A:Experimental source: strain Shiraz

Query Match 7.1%; Score 90.5; DB 2; Length 289;
Best Local Similarity 19.9%; Pred. No. 2.6;
Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

Qy 8 LLLVVISASATHEAQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGGACLENSTCDT 67
Db 59 LSTVIQSSDSKHEAAQ--AYADAGHCYKTSKAKEAISLCLEQA-----AYFLDNGRFNM 110
Qy 68 DQ-----MYDICKSFLYSAAKFDQTQGFVKESLKCIANGVTSKVFLAIRRCSTFOR 119
Db 111 AGKYKKEIAELYELSENFQAIYFEKAADIYQSEANTTAANQCNAKVAQPAQLEQYQK 170
Qy 120 MIAEVEECYSKLN-----VCSIAKRNPEAITEVVQL-----PNHFSNR 158
Db 171 ALQIYEDICRPSLNLLKYGKGLLNAGICQLCKGDVVAITNALDRYQEMDPTSGTR 230
Qy 159 YNRLVRSLECEDTSTVIRSLME 184
Db 231 EYKLLVDLAAAVDEEDVVKFTDAVKE 256

RESULT 10
T38690
probable regulatory protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C:Accession: T38690
R:Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21805
A:Accession: T38690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-783 <BRO>
A:Cross-references: UNIPROT:O14130; UNIPARC:UPI0000006AB27; EMBL:Z99568; PIDN:CABL6735.1
A:Experimental source: strain 972h-; cosmid c3c7
C:Genetics:
A:Gene: SPDB:SPAC3C7.04
A:Map position: 1
F:35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 7.1%; Score 90.5; DB 2; Length 783;
Best Local Similarity 23.3%; Pred. No. 8.6;
Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

QY 10 VLVISASATHEAEQNDVSVPKRSRV-----AAQNSAEVVRCLNSALQVGCAG----- 57
DB 535 IIMSRPVLHMKAKNSPRVDRINEDCILARHLISLVHLLQNHQSLSQVSPFDNYNT 594
QY 58 -----ACLENSTCDTGDGYDICKSFLYSAAKFTDQKAFVKESLKCI----- 99
DB 595 PSSALVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLPDAHLKG 650
QY 100 ----ANGVTSKV-FLAIRRCSTFORMIAVQ-----ECYSKLVNCSIAKRNPEAITEVV 149
DB 651 ARSDGNGNTSQSGFMA-----WQWIAEVSADPEKLMSPYKNSIOGGRNSLSLTGNA 704
QY 150 QLPNPHSNRYNR-----LVRSLLCEDEDVTSTIRDSLMKIGPNMA---SLPHILOTD 200
DB 705 NLGADV--FFPTDDTSFLLDHSKLDLLEKFASTLDPI---KTTPLDANDSSLNWNATD 760

RESULT 11
T01491
ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01491
R:Vayotskai, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, R.; D.; Li, Y.; Palm, C.U.; Shim, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.
A:Reference number: Z14334
A:Accession: T01491
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1126 <V3>
A:Cross-references: UNIPROT:064605; UNIPARC:UPI00000A614B; EMBL:AC003671; NID:g2833627;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP.F1707.15
A:Map position: 1
A:Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
F:756-1120/Domain: ubiquitin-protein ligase homology <UB1>

Query Match 7.1%; Score 89.5; DB 2; Length 1126;
Best Local Similarity 22.1%; Pred. No. 16;
Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

QY 14 SASATHEAEQNDVSVPKRSRVAAQNSAEVVRCLNSALQVGCAGFACLENSTCD----- 66
DB 412 SSETQKDASSELVARRK-----NCAEL---YNIFLQLP-----QSDLCNLCMLLGY 455
QY 67 ---TDGMYDICKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAE 123
DB 456 EGLSDKIYSLAGEVLKGLAAVDVTHRKFTFKSELSELASGLSSSTVRLATLTQGM--- 512
QY 124 VQECYSKLVNCSIAKRNPEAITEVVQLPNHFSNRYNRVLRSLLCEDEDVTSTIR----- 179
DB 513 -----SQNTCSMA---GASILRVQLVLSLTSTIDDSNVGTDKETDQEEQNMQLKV 562
QY 180 --DSLMEKIGPNNASLPHILOTDHCAQT 205
DB 563 ALEPLWQLGQCIS--MTQLQDHTAAT 588

RESULT 12
T08121
peroxidase (EC 1.11.1.7) - flax (fragment)
C:Species: Linum usitatissimum (flax)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08121
R:Omami, F.; Tyson, H.
submitted to the EMBL Data Library, February 1998

A:Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.

A:Reference number: Z16366
A:Accession: T08121
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-305 <OMA>
A:Cross-references: UNIPROT:O65029; UNIPARC:UPI00000AASD8; EMBL:AFO49881; NID:g2944416;
A:Experimental source: cv. Stormont Cirrus
C:Genetics:
A:Gene: PER4
C:Superfamily: peroxidase
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:23-103/Diulfide bonds: #status predicted
F:50/Active site: Arg #status predicted
F:54,181/Binding site: heme iron (His) (axial ligands) #status predicted
F:56-61/Diulfide bonds: #status predicted
F:109-301/Diulfide bonds: #status predicted
F:188-213/Diulfide bonds: #status predicted

Query Match 7.0%; Score 89; DB 2; Length 305;
Best Local Similarity 21.9%; Pred. No. 3.8;
Matches 57; Conservative 39; Mismatches 92; Indels 72; Gaps 15;

QY 11 LVISASATHEAEQNDVSVPKRSRVAAQNSAEVVRCLNSALQVGCAGFACLENSTCDTD 68
DB 65 LLLDDTAFTGEKN--AGPNQNSV---RGFDIITIKTRVEACNATVSCADILALAARD 119
QY 69 GMYDI-----CKSFLYSAAKFTDQKAFVKESLKCIANGVTSKVFLA----- 110
DB 120 GVLVGGGTWTVPLRRDARTASQSAANAQIPAPG---SSLGTTITNLTNKGLTARDVTI 176
QY 111 -----IRCSITFORMIAEVQECYSKLVN---CSIAKRN-PEA-----ITEVQLP 152
DB 177 LSGAHTTIGQARCTTFRQRI-----YNDTWIDPAPATRRGNCPOAGANLAPLDGTP 229
QY 153 NHFSNRYNRVLV--RSLLCEDEDVTST-IRDSLMKIGPNNASLPHILOTDHCAQ----- 204
DB 230 TQFDNRYQDILVARGLLHSQDELFNNGTQDALVRTYSNNAAT----FATDFAAAAVRMG 285
QY 205 -----THPRADFNRRRTN 217
DB 286 NISPLTGTNGEIRFNCRPN 305

RESULT 13
T45954
hypothetical protein F7J8.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45954
R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lein, H.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23018
A:Accession: T45954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-473 <BEV>
A:Cross-references: UNIPROT:O9LFC2; UNIPARC:UPI00000A92D2; EMBL:AL137189
A:Experimental source: cultivar Columbia; BAC clone F7J8
C:Genetics:
A:Map position: 5
A:Introns: 29/1; 428/3
A:Note: F7J8.120
C:Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

Query Match 6.9%; Score 88; DB 2; Length 473;
Best Local Similarity 22.6%; Pred. No. 7.8;
Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

QY 27 VSPKRSRVAAQNSAEVVRCLNSALQVGCAGFACLEN---STCD---TDGMYDICKS-FLY 79
DB 16 IDEEKNKVVLAEGAGTIVRLAKHRKSDPVTIGCLRNLVTSVVDMELDDETFACKOMLLY 75

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